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Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Date completed: 03-14-05
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PTO-1590 (9-90)

STIC-Biotech/ChemLib 87941

From: Schultz, James
Sent: Monday, March 03, 2003 11:08 AM
To: STIC-Biotech/ChemLib
Subject: sequence search request for 10/001,844

Hello,

I need a length limited nucleotide sequence search performed on SEQ ID NO:3 (1576 nt long) in the above entitled case, where the maximum size of the returned hit is no longer than 50 nucleotides.
Thank you very much,
Doug Schultz

J. Douglas Schultz, Ph.D
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(703) 308-9355
(703) 746-3973 (fax)
Office: CM1 12E18
Mail: CM1 11E12

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

Searcher:_____
Phone:_____
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Date Completed:_____
Searcher Prep/Review:_____
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TYPE OF SEARCH:
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
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Schultz, J.
10/001844
Seq. ID 3 w/ Interf

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 13, 2003, 21:54:09 ; Search time 3749 Seconds
(without alignments)
10569.368 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	143	21.6	1.4	50	17	US-09-306-333A-122	Sequence 122, App
	144	21.4	1.4	43	16	US-09-213-620B-4038	Sequence 4038, Ap
	145	21.4	1.4	43	16	US-09-213-620C-4038	Sequence 4038, Ap
	146	21.4	1.4	43	17	US-09-388-906A-8830	Sequence 8830, Ap
	147	21.4	1.4	44	7	US-08-369-832-344	Sequence 344, App
	148	21.4	1.4	45	35	US-09-946-374-151	Sequence 151, App
	149	21.4	1.4	45	38	US-10-006-041A-151	Sequence 151, App
	150	21.4	1.4	45	38	US-10-006-063A-151	Sequence 151, App
	151	21.4	1.4	45	38	US-10-006-116A-151	Sequence 151, App
	152	21.4	1.4	45	38	US-10-006-117A-151	Sequence 151, App
	153	21.4	1.4	45	38	US-10-006-130A-151	Sequence 151, App
	154	21.4	1.4	45	38	US-10-006-172A-151	Sequence 151, App
	155	21.4	1.4	45	38	US-10-006-485A-151	Sequence 151, App
	156	21.4	1.4	45	38	US-10-006-746A-151	Sequence 151, App
	157	21.4	1.4	45	38	US-10-006-768A-151	Sequence 151, App
	158	21.4	1.4	45	38	US-10-006-818A-151	Sequence 151, App
	159	21.4	1.4	45	38	US-10-006-856A-151	Sequence 151, App
	160	21.4	1.4	45	38	US-10-007-194A-151	Sequence 151, App
	161	21.4	1.4	45	38	US-10-007-236A-151	Sequence 151, App
	162	21.4	1.4	45	38	US-10-011-671A-151	Sequence 151, App
	163	21.4	1.4	45	38	US-10-011-692A-151	Sequence 151, App
	164	21.4	1.4	45	38	US-10-011-795A-151	Sequence 151, App
	165	21.4	1.4	45	38	US-10-011-795B-151	Sequence 151, App
	166	21.4	1.4	45	38	US-10-011-833A-151	Sequence 151, App
	167	21.4	1.4	45	38	US-10-012-064A-151	Sequence 151, App

	168	21.4	1.4	45	38	US-10-012-101B-151	Sequence 151, App
	169	21.4	1.4	45	38	US-10-012-121A-151	Sequence 151, App
	170	21.4	1.4	45	38	US-10-012-137A-151	Sequence 151, App
	171	21.4	1.4	45	38	US-10-012-149A-151	Sequence 151, App
	172	21.4	1.4	45	38	US-10-012-231A-151	Sequence 151, App
	173	21.4	1.4	45	38	US-10-012-237A-151	Sequence 151, App
	174	21.4	1.4	45	38	US-10-012-752A-151	Sequence 151, App
	175	21.4	1.4	45	38	US-10-012-753A-151	Sequence 151, App
	176	21.4	1.4	45	38	US-10-012-754A-151	Sequence 151, App
	177	21.4	1.4	45	38	US-10-012-755A-151	Sequence 151, App
	178	21.4	1.4	45	38	US-10-013-430A-151	Sequence 151, App
	179	21.4	1.4	45	38	US-10-013-906A-151	Sequence 151, App
	180	21.4	1.4	45	38	US-10-013-907A-151	Sequence 151, App
	181	21.4	1.4	45	38	US-10-013-909A-151	Sequence 151, App
	182	21.4	1.4	45	38	US-10-013-910A-151	Sequence 151, App
	183	21.4	1.4	45	38	US-10-013-911A-151	Sequence 151, App
	184	21.4	1.4	45	38	US-10-013-913A-151	Sequence 151, App
	185	21.4	1.4	45	38	US-10-013-915A-151	Sequence 151, App
	186	21.4	1.4	45	38	US-10-015-385A-151	Sequence 151, App
	187	21.4	1.4	45	38	US-10-015-386A-151	Sequence 151, App
	188	21.4	1.4	45	38	US-10-015-387A-151	Sequence 151, App
	189	21.4	1.4	45	38	US-10-015-388A-151	Sequence 151, App
	190	21.4	1.4	45	38	US-10-015-389A-151	Sequence 151, App
	191	21.4	1.4	45	38	US-10-015-390A-151	Sequence 151, App
	192	21.4	1.4	45	38	US-10-015-391A-151	Sequence 151, App
	193	21.4	1.4	45	38	US-10-015-393A-151	Sequence 151, App
	194	21.4	1.4	45	38	US-10-015-395A-151	Sequence 151, App
	195	21.4	1.4	45	38	US-10-015-480A-151	Sequence 151, App
	196	21.4	1.4	45	38	US-10-015-499A-151	Sequence 151, App
	197	21.4	1.4	45	38	US-10-015-519A-151	Sequence 151, App
	198	21.4	1.4	45	38	US-10-015-653A-151	Sequence 151, App
	199	21.4	1.4	45	38	US-10-015-671A-151	Sequence 151, App
	200	21.4	1.4	45	38	US-10-015-715A-151	Sequence 151, App
	201	21.4	1.4	45	38	US-10-015-822A-151	Sequence 151, App
	202	21.4	1.4	45	38	US-10-015-869A-151	Sequence 151, App
	203	21.4	1.4	45	38	US-10-017-306A-151	Sequence 151, App
	204	21.4	1.4	45	38	US-10-017-390A-151	Sequence 151, App
	205	21.4	1.4	45	38	US-10-017-407A-151	Sequence 151, App
	206	21.4	1.4	45	38	US-10-017-527A-151	Sequence 151, App
	207	21.4	1.4	45	38	US-10-017-610A-151	Sequence 151, App
	208	21.4	1.4	45	38	US-10-017-867A-151	Sequence 151, App
	209	21.4	1.4	45	38	US-10-020-063A-151	Sequence 151, App
c	210	21.4	1.4	47	1	PCT-US02-25943-54721	Sequence 54721, A
c	211	21.4	1.4	47	42	US-10-227-565-54721	Sequence 54721, A
	212	21.4	1.4	50	8	US-08-401-881A-889	Sequence 889, App
	213	21.4	1.4	50	8	US-08-401-881B-889	Sequence 889, App
	214	21.4	1.4	50	11	US-08-798-074-461	Sequence 461, App
	215	21.4	1.4	50	11	US-08-798-074-1485	Sequence 1485, Ap
	216	21.4	1.4	50	11	US-08-798-074B-461	Sequence 461, App
	217	21.4	1.4	50	11	US-08-798-074B-1485	Sequence 1485, Ap
	218	21.4	1.4	50	18	US-09-442-849B-640	Sequence 640, App
	219	21.4	1.4	50	18	US-09-443-199C-640	Sequence 640, App
	220	21.4	1.4	50	28	US-09-702-690-4	Sequence 4, Appli
c	221	21.4	1.4	50	29	US-09-755-374A-6512	Sequence 6512, Ap
	222	21.4	1.4	50	30	US-09-782-161-889	Sequence 889, App
	223	21.4	1.4	50	34	US-09-912-292-23514	Sequence 23514, A
	224	21.4	1.4	50	34	US-09-912-293-18701	Sequence 18701, A
	225	21.2	1.3	41	18	US-09-404-520-39161	Sequence 39161, A
	226	21.2	1.3	42	23	US-09-606-776-934	Sequence 934, App
	227	21.2	1.3	44	8	US-08-472-801-951	Sequence 951, App
	228	21.2	1.3	44	10	US-08-668-235-952	Sequence 952, App
	229	21.2	1.3	44	65	US-60-213-359-4527	Sequence 4527, Ap
	230	21.2	1.3	44	76	US-60-324-185-14828	Sequence 14828, A
c	231	21.2	1.3	45	17	US-09-306-333A-28	Sequence 28, Appl
	232	21.2	1.3	47	1	PCT-US02-25943-59274	Sequence 59274, A
	233	21.2	1.3	47	42	US-10-227-565-59274	Sequence 59274, A
	234	21.2	1.3	49	23	US-09-605-700-2406	Sequence 2406, Ap
c	235	21.2	1.3	50	5	US-08-196-362A-5685	Sequence 5685, Ap
c	236	21.2	1.3	50	5	US-08-196-362D-5685	Sequence 5685, Ap
c	237	21.2	1.3	50	5	US-08-196-362E-5685	Sequence 5685, Ap
c	238	21.2	1.3	50	5	US-08-196-362F-5685	Sequence 5685, Ap
c	239	21.2	1.3	50	5	US-08-196-362G-5685	Sequence 5685, Ap
c	240	21.2	1.3	50	17	US-09-306-333A-27	Sequence 27, Appl
c	241	21.2	1.3	50	29	US-09-755-374A-2450	Sequence 2450, Ap
c	242	21	1.3	39	1	PCT-US02-25943-35825	Sequence 35825, A
c	243	21	1.3	39	42	US-10-227-565-35825	Sequence 35825, A
c	244	21	1.3	47	1	PCT-US02-25943-62619	Sequence 62619, A
	245	21	1.3	47	29	US-09-724-866-9247	Sequence 9247, Ap
	246	21	1.3	47	29	US-09-724-866A-9247	Sequence 9247, Ap
	247	21	1.3	47	41	US-10-170-097-935	Sequence 935, App
	248	21	1.3	47	41	US-10-170-097-1096	Sequence 1096, Ap
c	249	21	1.3	47	42	US-10-227-565-62619	Sequence 62619, A
	250	21	1.3	47	61	US-60-171-432-9247	Sequence 9247, Ap
	251	21	1.3	50	1	PCT-US02-25943-35824	Sequence 35824, A
c	252	21	1.3	50	8	US-08-475-228-374	Sequence 374, App
c	253	21	1.3	50	8	US-08-482-080-374	Sequence 374, App
c	254	21	1.3	50	11	US-08-781-986A-2153	Sequence 2153, Ap
c	255	21	1.3	50	13	US-08-956-171-2153	Sequence 2153, Ap
c	256	21	1.3	50	13	US-08-956-171B-2153	Sequence 2153, Ap
c	257	21	1.3	50	13	US-08-956-171C-2153	Sequence 2153, Ap
c	258	21	1.3	50	13	US-08-956-171E-2153	Sequence 2153, Ap
c	259	21	1.3	50	29	US-09-755-374A-876	Sequence 876, App
	260	21	1.3	50	29	US-09-755-374A-14682	Sequence 14682, A
	261	21	1.3	50	29	US-09-755-374A-19358	Sequence 19358, A
c	262	21	1.3	50	29	US-09-755-374A-27994	Sequence 27994, A
c	263	21	1.3	50	37	US-09-993-346-374	Sequence 374, App
	264	21	1.3	50	42	US-10-227-565-35824	Sequence 35824, A
c	265	20.8	1.3	38	1	PCT-US02-25943-14120	Sequence 14120, A
c	266	20.8	1.3	38	42	US-10-227-565-14120	Sequence 14120, A
c	267	20.8	1.3	40	1	PCT-US02-25940-7237	Sequence 7237, Ap
c	268	20.8	1.3	40	17	US-09-306-333A-29	Sequence 29, Appl
c	269	20.8	1.3	40	42	US-10-227-563-7237	Sequence 7237, Ap
	270	20.8	1.3	43	18	US-09-445-375A-24	Sequence 24, Appl
	271	20.8	1.3	43	38	US-10-016-686-6	Sequence 6, Appli
	272	20.8	1.3	43	39	US-10-060-585-12	Sequence 12, Appl
	273	20.8	1.3	43	40	US-10-104-522-24	Sequence 24, Appl
	274	20.8	1.3	45	40	US-10-135-984-6	Sequence 6, Appli
	275	20.8	1.3	46	22	US-09-584-852-2184	Sequence 2184, Ap
	276	20.8	1.3	46	40	US-10-135-984-4	Sequence 4, Appli
c	277	20.8	1.3	46	40	US-10-135-984-5	Sequence 5, Appli
c	278	20.8	1.3	46	40	US-10-135-984-7	Sequence 7, Appli
c	279	20.8	1.3	47	18	US-09-445-375A-8	Sequence 8, Appli
c	280	20.8	1.3	47	38	US-10-016-686-16	Sequence 16, Appl
c	281	20.8	1.3	47	39	US-10-060-585-13	Sequence 13, Appl
c	282	20.8	1.3	47	40	US-10-104-522-8	Sequence 8, Appli
	283	20.8	1.3	47	41	US-10-170-097-934	Sequence 934, App
	284	20.8	1.3	47	65	US-60-216-745-2568	Sequence 2568, Ap
c	285	20.8	1.3	48	8	US-08-478-097-33	Sequence 33, Appl
c	286	20.8	1.3	48	18	US-09-496-398-33	Sequence 33, Appl
c	287	20.8	1.3	49	1	PCT-US02-25943-26757	Sequence 26757, A
c	288	20.8	1.3	49	42	US-10-227-565-26757	Sequence 26757, A
c	289	20.8	1.3	49	69	US-60-252-833-32799	Sequence 32799, A
	290	20.8	1.3	50	29	US-09-755-374A-19830	Sequence 19830, A
c	291	20.8	1.3	50	29	US-09-755-374A-27182	Sequence 27182, A
	292	20.8	1.3	50	29	US-09-755-374A-27977	Sequence 27977, A
	293	20.6	1.3	27	40	US-10-108-969-4	Sequence 4, Appli
	294	20.6	1.3	38	16	US-09-213-620B-1242	Sequence 1242, Ap
	295	20.6	1.3	38	16	US-09-213-620C-1242	Sequence 1242, Ap
	296	20.6	1.3	38	18	US-09-411-999-364	Sequence 364, App
	297	20.6	1.3	39	21	US-09-548-954A-1120	Sequence 1120, Ap
	298	20.6	1.3	39	21	US-09-548-954B-1120	Sequence 1120, Ap
c	299	20.6	1.3	40	1	PCT-US02-25940-20998	Sequence 20998, A
c	300	20.6	1.3	40	42	US-10-227-563-20998	Sequence 20998, A
	301	20.6	1.3	41	1	PCT-US02-12063-251	Sequence 251, App
	302	20.6	1.3	41	40	US-10-126-022-251	Sequence 251, App
	303	20.6	1.3	45	4	US-08-086-411-1	Sequence 1, Appli
c	304	20.6	1.3	45	38	US-10-014-282-22	Sequence 22, Appl
c	305	20.6	1.3	47	1	PCT-US02-25943-48985	Sequence 48985, A
c	306	20.6	1.3	47	42	US-10-227-565-48985	Sequence 48985, A
	307	20.6	1.3	50	11	US-08-790-774-9334	Sequence 9334, Ap
c	308	20.6	1.3	50	11	US-08-798-074-4266	Sequence 4266, Ap
c	309	20.6	1.3	50	11	US-08-798-074B-4266	Sequence 4266, Ap
c	310	20.6	1.3	50	29	US-09-726-173A-1202	Sequence 1202, Ap
	311	20.6	1.3	50	29	US-09-755-374A-12538	Sequence 12538, A
	312	20.4	1.3	30	7	US-08-301-013-17	Sequence 17, Appl
c	313	20.4	1.3	30	26	US-09-669-187A-1096	Sequence 1096, Ap

c 314	20.4	1.3	30	40	US-10-144-360-4	Sequence 4, Appli
c 315	20.4	1.3	32	1	PCT-US02-25940-4004	Sequence 4004, Ap
c 316	20.4	1.3	32	40	US-10-144-360-5	Sequence 5, Appli
c 317	20.4	1.3	32	42	US-10-227-563-4004	Sequence 4004, Ap
c 318	20.4	1.3	34	40	US-10-144-360-6	Sequence 6, Appli
c 319	20.4	1.3	35	26	US-09-669-187A-771	Sequence 771, App
c 320	20.4	1.3	35	30	US-09-776-479-771	Sequence 771, App
c 321	20.4	1.3	35	33	US-09-888-326-172	Sequence 172, App
c 322	20.4	1.3	35	38	US-10-017-995-771	Sequence 771, App
c 323	20.4	1.3	35	40	US-10-112-653-744	Sequence 744, App
324	20.4	1.3	36	5	US-08-131-104-3	Sequence 3, Appli
c 325	20.4	1.3	36	40	US-10-144-360-7	Sequence 7, Appli
c 326	20.4	1.3	38	40	US-10-144-360-8	Sequence 8, Appli
c 327	20.4	1.3	39	1	PCT-US02-25943-47774	Sequence 47774, A
c 328	20.4	1.3	39	42	US-10-227-565-47774	Sequence 47774, A
c 329	20.4	1.3	40	1	PCT-US97-19596-37	Sequence 37, Appl
c 330	20.4	1.3	40	1	PCT-US97-19596A-37	Sequence 37, Appl
c 331	20.4	1.3	40	3	US-07-969-192A-1	Sequence 1, Appli
c 332	20.4	1.3	40	13	US-08-962-012-37	Sequence 37, Appl
c 333	20.4	1.3	40	40	US-10-144-360-9	Sequence 9, Appli
334	20.4	1.3	41	1	PCT-US02-25940-14922	Sequence 14922, A
335	20.4	1.3	41	4	US-08-084-033A-14	Sequence 14, Appl
336	20.4	1.3	41	13	US-08-930-589-14	Sequence 14, Appl
337	20.4	1.3	41	18	US-09-404-520-31285	Sequence 31285, A
338	20.4	1.3	41	38	US-10-027-961A-14	Sequence 14, Appl
c 339	20.4	1.3	41	40	US-10-144-360-20	Sequence 20, Appl
340	20.4	1.3	41	42	US-10-227-563-14922	Sequence 14922, A
c 341	20.4	1.3	42	39	US-10-061-071-76	Sequence 76, Appl
342	20.4	1.3	44	5	US-08-131-104-2	Sequence 2, Appli
c 343	20.4	1.3	45	1	PCT-US02-25940-12335	Sequence 12335, A
c 344	20.4	1.3	45	42	US-10-227-563-12335	Sequence 12335, A
c 345	20.4	1.3	46	1	PCT-US02-25943-40405	Sequence 40405, A
c 346	20.4	1.3	46	42	US-10-227-565-40405	Sequence 40405, A
c 347	20.4	1.3	47	6	US-08-233-596A-7	Sequence 7, Appli
348	20.4	1.3	48	1	PCT-US02-25940-11618	Sequence 11618, A
349	20.4	1.3	48	42	US-10-227-563-11618	Sequence 11618, A
350	20.4	1.3	49	29	US-09-740-002-9	Sequence 9, Appli
351	20.4	1.3	50	11	US-08-781-986A-5127	Sequence 5127, Ap
352	20.4	1.3	50	13	US-08-956-171-5127	Sequence 5127, Ap
353	20.4	1.3	50	13	US-08-956-171B-5127	Sequence 5127, Ap
354	20.4	1.3	50	13	US-08-956-171C-5127	Sequence 5127, Ap
355	20.4	1.3	50	13	US-08-956-171E-5127	Sequence 5127, Ap
356	20.4	1.3	50	28	US-09-702-690-3	Sequence 3, Appli
c 357	20.4	1.3	50	29	US-09-755-374A-7332	Sequence 7332, Ap
c 358	20.4	1.3	50	29	US-09-755-374A-14160	Sequence 14160, A
c 359	20.4	1.3	50	29	US-09-755-374A-16320	Sequence 16320, A
c 360	20.4	1.3	50	29	US-09-755-374A-27180	Sequence 27180, A
361	20.2	1.3	25	17	US-09-396-196F-67178	Sequence 67178, A
362	20.2	1.3	25	17	US-09-396-196G-67178	Sequence 67178, A
c 363	20.2	1.3	34	1	PCT-US02-25943-19012	Sequence 19012, A
c 364	20.2	1.3	34	1	PCT-US02-25943-39117	Sequence 39117, A
c 365	20.2	1.3	34	42	US-10-227-565-19012	Sequence 19012, A
c 366	20.2	1.3	34	42	US-10-227-565-39117	Sequence 39117, A
367	20.2	1.3	41	18	US-09-404-520-32345	Sequence 32345, A
c 368	20.2	1.3	42	1	PCT-US02-25943-14679	Sequence 14679, A
c 369	20.2	1.3	42	42	US-10-227-565-14679	Sequence 14679, A
370	20.2	1.3	44	69	US-60-253-654-27120	Sequence 27120, A
371	20.2	1.3	44	69	US-60-255-592-27120	Sequence 27120, A
c 372	20.2	1.3	45	1	PCT-US02-25940-22163	Sequence 22163, A
c 373	20.2	1.3	45	42	US-10-227-563-22163	Sequence 22163, A
c 374	20.2	1.3	46	1	PCT-US02-25943-13749	Sequence 13749, A
375	20.2	1.3	46	8	US-08-475-228-85	Sequence 85, Appl
376	20.2	1.3	46	8	US-08-482-080-85	Sequence 85, Appl
377	20.2	1.3	46	16	US-09-230-930B-1	Sequence 1, Appli
c 378	20.2	1.3	46	16	US-09-230-930B-1	Sequence 1, Appli
379	20.2	1.3	46	37	US-09-993-346-85	Sequence 85, Appl
c 380	20.2	1.3	46	42	US-10-227-565-13749	Sequence 13749, A
c 381	20.2	1.3	47	6	US-08-292-686B-48	Sequence 48, Appl
c 382	20.2	1.3	47	10	US-08-601-209A-67	Sequence 67, Appl
c 383	20.2	1.3	48	22	US-09-577-410-6513	Sequence 6513, Ap
384	20.2	1.3	48	38	US-10-016-686-35	Sequence 35, Appl
385	20.2	1.3	48	39	US-10-072-152-32	Sequence 32, Appl
c 386	20.2	1.3	49	1	PCT-US02-25943-1156	Sequence 1156, Ap
c 387	20.2	1.3	49	8	US-08-472-801-1459	Sequence 1459, Ap
c 388	20.2	1.3	49	10	US-08-668-235-1459	Sequence 1459, Ap
c 389	20.2	1.3	49	42	US-10-227-565-1156	Sequence 1156, Ap
c 390	20.2	1.3	50	7	US-08-361-811-107	Sequence 107, App
c 391	20.2	1.3	50	7	US-08-381-478-144	Sequence 144, App
c 392	20.2	1.3	50	9	US-08-535-025-144	Sequence 144, App
c 393	20.2	1.3	50	9	US-08-591-919-144	Sequence 144, App
c 394	20.2	1.3	50	9	US-08-592-007-144	Sequence 144, App
c 395	20.2	1.3	50	9	US-08-592-027-144	Sequence 144, App
c 396	20.2	1.3	50	9	US-08-592-131-144	Sequence 144, App
c 397	20.2	1.3	50	13	US-08-964-039-144	Sequence 144, App
c 398	20.2	1.3	50	25	US-09-642-058-242	Sequence 242, App
399	20.2	1.3	50	29	US-09-755-374A-8544	Sequence 8544, Ap
400	20.2	1.3	50	29	US-09-755-374A-26916	Sequence 26916, A
c 401	20.2	1.3	50	32	US-09-846-038-821	Sequence 821, App
402	20	1.3	30	1	PCT-US02-25943-15189	Sequence 15189, A
403	20	1.3	30	42	US-10-227-565-15189	Sequence 15189, A
c 404	20	1.3	32	14	US-09-063-778-31	Sequence 31, Appl
c 405	20	1.3	32	23	US-09-617-545-31	Sequence 31, Appl
c 406	20	1.3	32	40	US-10-147-463-31	Sequence 31, Appl
407	20	1.3	36	1	PCT-US02-25940-8624	Sequence 8624, Ap
408	20	1.3	36	42	US-10-227-563-8624	Sequence 8624, Ap
c 409	20	1.3	38	1	PCT-US02-25940-6205	Sequence 6205, Ap
c 410	20	1.3	38	1	PCT-US02-25940-14921	Sequence 14921, A
c 411	20	1.3	38	42	US-10-227-563-6205	Sequence 6205, Ap
c 412	20	1.3	38	42	US-10-227-563-14921	Sequence 14921, A
413	20	1.3	40	18	US-09-411-999-60	Sequence 60, Appl
c 414	20	1.3	41	18	US-09-404-520-34796	Sequence 34796, A
c 415	20	1.3	41	36	US-09-953-198-338	Sequence 338, App
c 416	20	1.3	41	36	US-09-953-198-684	Sequence 684, App
417	20	1.3	45	1	PCT-US00-11500-35	Sequence 35, Appl
418	20	1.3	45	28	US-09-709-238-122	Sequence 122, App
419	20	1.3	45	32	US-09-857-723-202	Sequence 202, App
420	20	1.3	45	35	US-09-941-992-122	Sequence 122, App
421	20	1.3	45	37	US-09-989-279-122	Sequence 122, App
422	20	1.3	45	37	US-09-989-293A-122	Sequence 122, App
423	20	1.3	45	37	US-09-989-328-122	Sequence 122, App
424	20	1.3	45	37	US-09-989-721-122	Sequence 122, App
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426	20	1.3	45	37	US-09-989-723-122	Sequence 122, App
427	20	1.3	45	37	US-09-989-724-122	Sequence 122, App
428	20	1.3	45	37	US-09-989-725-122	Sequence 122, App
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437	20	1.3	45	37	US-09-989-735-122	Sequence 122, App
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441	20	1.3	45	37	US-09-990-437-122	Sequence 122, App
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449	20	1.3	45	37	US-09-990-456-122	Sequence 122, App
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452	20	1.3	45	37	US-09-990-726-122	Sequence 122, App
453	20	1.3	45	37	US-09-991-073-122	Sequence 122, App
454	20	1.3	45	37	US-09-991-150-122	Sequence 122, App
455	20	1.3	45	37	US-09-991-157-122	Sequence 122, App
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	524	19.8	1.3	39	1	PCT-US02-25943-33117
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Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 122, App
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Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 122, App
Sequence 9, Appli
Sequence 35, Appl
Sequence 122, App
Sequence 2396, Ap
Sequence 39936, A
Sequence 11039, A
Sequence 2396, Ap
Sequence 27146, A
Sequence 39165, A
Sequence 776, App
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 27146, A
Sequence 39165, A
Sequence 23442, A
Sequence 23442, A
Sequence 134, App
Sequence 56525, A
Sequence 13, Appl
Sequence 12964, A
Sequence 12964, A
Sequence 1888, Ap
Sequence 16572, A
Sequence 16574, A
Sequence 25791, A
Sequence 56525, A
Sequence 62926, A
Sequence 62926, A
Sequence 111223,
Sequence 111223,
Sequence 388, App
Sequence 389, App
Sequence 33117, A
Sequence 33117, A
Sequence 24, Appl
Sequence 26587, A
Sequence 34886, A
Sequence 35503, A
Sequence 20684, A
Sequence 206, App
Sequence 20684, A

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c	546	19.8	1.3	47	42	US-10-227-565-60375
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c	548	19.8	1.3	49	29	US-09-724-866A-10697
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	551	19.8	1.3	50	1	PCT-US02-25942-11692
	552	19.8	1.3	50	1	PCT-US02-25942-11694
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	571	19.6	1.2	41	18	US-09-404-520-30544
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	583	19.6	1.2	44	42	US-10-227-563-12751
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	587	19.6	1.2	46	30	US-09-763-037-8
	588	19.6	1.2	47	1	PCT-US02-25943-30505
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	592	19.6	1.2	49	28	US-09-704-424-22217
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	594	19.6	1.2	50	1	PCT-US02-25943-11895
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	596	19.6	1.2	50	6	US-08-220-661A-57
	597	19.6	1.2	50	6	US-08-220-661B-57
	598	19.6	1.2	50	6	US-08-220-662-57
	599	19.6	1.2	50	11	US-08-798-074-495
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Sequence 18488, A
Sequence 4257, Ap
Sequence 4257, Ap
Sequence 18488, A
Sequence 30397, A
Sequence 30397, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 462, App
Sequence 28002, A
Sequence 60375, A
Sequence 462, App
Sequence 28002, A
Sequence 60375, A
Sequence 10697, A
Sequence 10697, A
Sequence 10697, A
Sequence 9874, Ap
Sequence 11692, A
Sequence 11694, A
Sequence 2374, Ap
Sequence 14800, A
Sequence 14802, A
Sequence 17394, A
Sequence 9874, Ap
Sequence 11692, A
Sequence 11694, A
Sequence 43543, A
Sequence 43543, A
Sequence 5013, Ap
Sequence 49297, A
Sequence 49297, A
Sequence 5013, Ap
Sequence 16824, A
Sequence 16824, A
Sequence 12752, A
Sequence 184, App
Sequence 184, App
Sequence 30544, A
Sequence 38730, A
Sequence 12752, A
Sequence 29014, A
Sequence 6376, Ap
Sequence 1382, Ap
Sequence 1382, Ap
Sequence 6376, Ap
Sequence 12751, A
Sequence 30167, A
Sequence 438, App
Sequence 439, App
Sequence 12751, A
Sequence 30167, A
Sequence 43763, A
Sequence 9, Appli
Sequence 8, Appli
Sequence 30505, A
Sequence 30505, A
Sequence 3708, Ap
Sequence 46, Appl
Sequence 22217, A
Sequence 181, App
Sequence 11895, A
Sequence 19, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 495, App
Sequence 495, App
Sequence 712, App
Sequence 672, App
Sequence 8092, Ap
Sequence 12398, A
Sequence 14266, A

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c 610	19.6	1.2	50	40	US-10-131-827-181	Sequence 181, App
c 611	19.6	1.2	50	40	US-10-131-831-181	Sequence 181, App
612	19.6	1.2	50	42	US-10-227-565-11895	Sequence 11895, A
c 613	19.6	1.2	50	48	US-60-047-802-712	Sequence 712, App
c 614	19.4	1.2	25	17	US-09-396-196F-62925	Sequence 62925, A
615	19.4	1.2	25	17	US-09-396-196F-87943	Sequence 87943, A
c 616	19.4	1.2	25	17	US-09-396-196G-62925	Sequence 62925, A
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623	19.4	1.2	29	42	US-10-227-565-28563	Sequence 28563, A
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c 625	19.4	1.2	30	42	US-10-227-565-58398	Sequence 58398, A
626	19.4	1.2	31	1	PCT-US02-25943-30422	Sequence 30422, A
627	19.4	1.2	31	42	US-10-227-565-30422	Sequence 30422, A
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629	19.4	1.2	38	77	US-60-334-904-185	Sequence 185, App
630	19.4	1.2	39	28	US-09-704-424-33212	Sequence 33212, A
c 631	19.4	1.2	40	8	US-08-472-801-510	Sequence 510, App
c 632	19.4	1.2	40	10	US-08-668-235-511	Sequence 511, App
c 633	19.4	1.2	42	1	PCT-US02-25943-43897	Sequence 43897, A
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635	19.4	1.2	43	1	PCT-US02-25940-11707	Sequence 11707, A
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637	19.4	1.2	43	11	US-08-728-463-245	Sequence 245, App
638	19.4	1.2	43	11	US-08-728-463B-245	Sequence 245, App
639	19.4	1.2	43	29	US-09-724-965-245	Sequence 245, App
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c 643	19.4	1.2	45	1	PCT-US02-25940-25167	Sequence 25167, A
c 644	19.4	1.2	45	1	PCT-US02-25943-13816	Sequence 13816, A
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Sequence 903, App
Sequence 903, App
Sequence 405, App
Sequence 512, App
Sequence 20906, A
Sequence 4723, Ap
Sequence 3427, Ap
Sequence 46863, A
Sequence 6952, Ap
Sequence 3964, Ap
Sequence 1684, Ap
Sequence 2002, Ap
Sequence 2004, Ap
Sequence 5836, Ap
Sequence 6533, Ap
Sequence 7628, Ap
Sequence 11220, A
Sequence 13698, A
Sequence 14164, A
Sequence 17356, A
Sequence 17358, A
Sequence 3427, Ap
Sequence 3427, Ap
Sequence 46863, A
Sequence 132, App
Sequence 16, Appl
Sequence 21, Appl
Sequence 5, Appli
Sequence 9, Appli
Sequence 8, Appli
Sequence 11708, A
Sequence 11, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 36, Appl
Sequence 11708, A
Sequence 2516, Ap
Sequence 2516, Ap
Sequence 69, Appl
Sequence 15, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 5318, Ap
Sequence 141, App
Sequence 8, Appli
Sequence 5318, Ap
Sequence 24521, A
Sequence 9516, Ap
Sequence 16, Appl
Sequence 12, Appl
Sequence 24521, A
Sequence 9516, Ap
Sequence 405, App
Sequence 32, Appl
Sequence 31847, A
Sequence 105, App
Sequence 139, App
Sequence 405, App
Sequence 2589, Ap
Sequence 6782, Ap
Sequence 42641, A
Sequence 6782, Ap
Sequence 21935, A
Sequence 1530, Ap

Sequence 21935, A
Sequence 11650, A
Sequence 40980, A
Sequence 38, Appl
Sequence 11650, A
Sequence 40980, A
Sequence 8798, Ap
Sequence 45868, A
Sequence 7, Appli
Sequence 13, Appl
Sequence 14, Appl
Sequence 7, Appli
Sequence 7, Appli
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Sequence 7, Appli
Sequence 33360, A
Sequence 37902, A
Sequence 8798, Ap
Sequence 45868, A
Sequence 3190, Ap
Sequence 11628, A
Sequence 10, Appl
Sequence 3190, Ap
Sequence 11628, A
Sequence 10, Appl
Sequence 55159, A
Sequence 45, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 55159, A
Sequence 25020, A
Sequence 4503, Ap
Sequence 31210, A
Sequence 25020, A
Sequence 26021, A
Sequence 42513, A
Sequence 32799, A
Sequence 4902, Ap
Sequence 32194, A
Sequence 458, App
Sequence 5790, Ap
Sequence 5792, Ap
Sequence 8054, Ap
Sequence 9948, Ap
Sequence 10086, A
Sequence 14161, A
Sequence 17060, A
Sequence 17088, A
Sequence 21930, A
Sequence 21932, A
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Sequence 1557, Ap

c	898	18.8	1.2	36	10	US-08-668-235-1557
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c	901	18.8	1.2	38	42	US-10-227-565-18344
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c	905	18.8	1.2	39	40	US-10-100-679-8
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c	926	18.8	1.2	41	18	US-09-404-520-34360
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c	933	18.8	1.2	42	7	US-08-300-726A-43
c	934	18.8	1.2	42	29	US-09-747-377-486
	935	18.8	1.2	42	32	US-09-833-203-8
c	936	18.8	1.2	42	32	US-09-833-203-9
c	937	18.8	1.2	42	38	US-10-035-832-946
c	938	18.8	1.2	42	40	US-10-105-613-486
	939	18.8	1.2	42	40	US-10-121-258-65
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	942	18.8	1.2	43	1	PCT-US02-25940-11913
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	944	18.8	1.2	43	8	US-08-463-519-7
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	947	18.8	1.2	43	42	US-10-227-565-17427
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	951	18.8	1.2	44	9	US-08-596-382-18
c	952	18.8	1.2	44	18	US-09-404-520-33866
	953	18.8	1.2	44	23	US-09-605-700-10920
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	956	18.8	1.2	45	18	US-09-404-520-41743
	957	18.8	1.2	45	32	US-09-847-662-640
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c	968	18.8	1.2	46	42	US-10-227-565-15255
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c	970	18.8	1.2	46	69	US-60-255-592-19101

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	973	18.8	1.2	47	1	PCT-US02-25943-15799
	974	18.8	1.2	47	1	PCT-US02-25943-27963
	975	18.8	1.2	47	1	PCT-US02-25943-28002
c	976	18.8	1.2	47	9	US-08-503-525-51
c	977	18.8	1.2	47	16	US-09-215-712-51
c	978	18.8	1.2	47	16	US-09-215-989-51
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	980	18.8	1.2	47	42	US-10-227-565-1527
	981	18.8	1.2	47	42	US-10-227-565-13316
	982	18.8	1.2	47	42	US-10-227-565-15799
	983	18.8	1.2	47	42	US-10-227-565-27963
	984	18.8	1.2	47	42	US-10-227-565-28002
	985	18.8	1.2	47	65	US-60-216-745-1297
	986	18.8	1.2	47	69	US-60-252-833-18788
c	987	18.8	1.2	48	1	PCT-US02-25943-18755
	988	18.8	1.2	48	1	PCT-US02-25943-22358
	989	18.8	1.2	48	1	PCT-US99-06554-2
c	990	18.8	1.2	48	6	US-08-224-010A-25
c	991	18.8	1.2	48	6	US-08-224-010B-25
	992	18.8	1.2	48	7	US-08-351-414-11
c	993	18.8	1.2	48	17	US-09-399-932-3610
c	994	18.8	1.2	48	42	US-10-227-565-18755
	995	18.8	1.2	48	42	US-10-227-565-22358
c	996	18.8	1.2	50	1	PCT-US01-47856-1563
	997	18.8	1.2	50	1	PCT-US01-47856-4569
	998	18.8	1.2	50	1	PCT-US02-25943-17406
	999	18.8	1.2	50	1	PCT-US02-25943-64136
	1000	18.8	1.2	50	1	PCT-US02-25943-64137

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Sequence 28002, A
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Sequence 28002, A
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Sequence 11, Appl
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Sequence 64136, A
Sequence 64137, A

ALIGNMENTS

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RESULT 1
US-09-590-211-9
; Sequence 9, Application US/09590211
; GENERAL INFORMATION:
;  APPLICANT: Rouleau, Guy A.
;  APPLICANT:  Brais, Bernard
;  TITLE OF INVENTION: Short GCG Expansions in the PAB II Gene
;  TITLE OF INVENTION:  for Oculopharyngeal Muscular Dystrophy and Diagnostic
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: 3028.1000-000
;  CURRENT APPLICATION NUMBER: US/09/590,211
;  CURRENT FILING DATE:  2000-06-08
;  PRIOR APPLICATION NUMBER: PCT/CA98/01133
;  PRIOR FILING DATE: 1998-12-07
;  PRIOR APPLICATION NUMBER: 2,218,199
;  PRIOR FILING DATE: 1997-12-09
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 45
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-590-211-9

  Query Match             2.0%;  Score 31.8;  DB 22;  Length 45;
  Best Local Similarity   83.7%;  Pred. No. 1.7e+05;
  Matches   36;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    1343 GGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCA 1385
           ||||| | | |||||||||| | | |||| ||||||||||||
Db       3 GGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCA 45


RESULT 2
US-09-590-211A-9
; Sequence 9, Application US/09590211A
; GENERAL INFORMATION:
;  APPLICANT: Rouleau, Guy A.
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 ;  APPLICANT:  Brais, Bernard
 ;  TITLE OF INVENTION: SHORT GCG EXPANSIONS IN THE PAB II GENE
 ;  TITLE OF INVENTION:  FOR OCULOPHARYNGEAL MUSCULAR DYSTROPHY AND DIAGNOSTIC THereof
 ;  FILE REFERENCE: 3028.1000-000
 ;  CURRENT APPLICATION NUMBER: US/09/590,211A
 ;  CURRENT FILING DATE:  2000-06-08
 ;  PRIOR APPLICATION NUMBER: PCT/CA98/01133
 ;  PRIOR FILING DATE: 1998-12-07
 ;  PRIOR APPLICATION NUMBER: 2,218,199
 ;  PRIOR FILING DATE: 1997-12-09
 ;  NUMBER OF SEQ ID NOS: 21
 ;  SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 9
 ;   LENGTH: 45
 ;   TYPE: DNA
 ;   ORGANISM: Homo sapiens
US-09-590-211A-9

  Query Match             2.0%;  Score 31.8;  DB 22;  Length 45;
  Best Local Similarity   83.7%;  Pred. No. 1.7e+05;
  Matches   36;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   1343 GGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCA 1385
           ||||| | | |||||||||| | | |||| ||||||||||||
Db      3 GGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCA 45


RESULT 3
US-09-782-650-16
; Sequence 16, Application US/09782650
; GENERAL INFORMATION:
 ;  APPLICANT: Levine, Arnold J.
 ;  APPLICANT:  Mitterer, Artur
 ;  APPLICANT:  Falkner, Falko-Guenter
 ;  APPLICANT:  Scheiflinger, Friedrich
 ;  APPLICANT:  Dorner, Friedrich
 ;  APPLICANT:  Edwards LifeSciences Corporation
 ;  TITLE OF INVENTION: Targeted Angiogenesis
 ;  FILE REFERENCE: 20553D-000611US
 ;  CURRENT APPLICATION NUMBER: US/09/782,650
 ;  CURRENT FILING DATE:  2001-02-12
 ;  PRIOR APPLICATION NUMBER: US 09/324,079
 ;  PRIOR FILING DATE: 1999-06-01
 ;  PRIOR APPLICATION NUMBER: US 09/327,045
 ;  PRIOR FILING DATE: 1999-06-07
 ;  PRIOR APPLICATION NUMBER: PCT/US00/14988
 ;  PRIOR FILING DATE: 2000-05-31
 ;  NUMBER OF SEQ ID NOS: 24
 ;  SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 16
 ;   LENGTH: 50
 ;   TYPE: DNA
 ;   ORGANISM: Artificial Sequence
 ;   FEATURE:
 ;   OTHER INFORMATION: Description of Artificial Sequence:annealed
 ;   OTHER INFORMATION: oligonucleotide
US-09-782-650-16

  Query Match             2.0%;  Score 31.4;  DB 30;  Length 50;
  Best Local Similarity   85.4%;  Pred. No. 1.9e+05;
  Matches   35;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   1341 GCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGC 1381
           ||||||| | |||||||||||| | | |||| |||||||||
Db      7 GCGGCGGCGGCAGCGGCGGCGGCGGCAGCGGCGGCGGCGGC 47


RESULT 4
US-09-590-211-8
; Sequence 8, Application US/09590211
; GENERAL INFORMATION:
 ;  APPLICANT: Rouleau, Guy A.
 ;  APPLICANT:  Brais, Bernard
 ;  TITLE OF INVENTION: Short GCG Expansions in the PAB II Gene
 ;  TITLE OF INVENTION:  for Oculopharyngeal Muscular Dystrophy and Diagnostic
 ;  TITLE OF INVENTION:  Thereof
 ;  FILE REFERENCE: 3028.1000-000
 ;  CURRENT APPLICATION NUMBER: US/09/590,211
 ;  CURRENT FILING DATE:  2000-06-08
 ;  PRIOR APPLICATION NUMBER: PCT/CA98/01133
 ;  PRIOR FILING DATE: 1998-12-07
 ;  PRIOR APPLICATION NUMBER: 2,218,199
 ;  PRIOR FILING DATE: 1997-12-09
 ;  NUMBER OF SEQ ID NOS: 21
 ;  SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 8
 ;   LENGTH: 42
 ;   TYPE: DNA
 ;   ORGANISM: Homo sapiens
US-09-590-211-8

  Query Match             1.8%;  Score 28.8;  DB 22;  Length 42;
  Best Local Similarity   82.5%;  Pred. No. 5e+05;
  Matches   33;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   1346 GGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCA 1385
           || | | |||||||||| | | |||| ||||||||||||
Db      3 GGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCA 42


RESULT 5
US-09-590-211A-8
; Sequence 8, Application US/09590211A
; GENERAL INFORMATION:
 ;  APPLICANT: Rouleau, Guy A.
 ;  APPLICANT:  Brais, Bernard
 ;  TITLE OF INVENTION: SHORT GCG EXPANSIONS IN THE PAB II GENE
 ;  TITLE OF INVENTION:  FOR OCULOPHARYNGEAL MUSCULAR DYSTROPHY AND DIAGNOSTIC THer
 ;  FILE REFERENCE: 3028.1000-000
 ;  CURRENT APPLICATION NUMBER: US/09/590,211A
 ;  CURRENT FILING DATE:  2000-06-08
 ;  PRIOR APPLICATION NUMBER: PCT/CA98/01133
 ;  PRIOR FILING DATE: 1998-12-07
 ;  PRIOR APPLICATION NUMBER: 2,218,199
 ;  PRIOR FILING DATE: 1997-12-09
 ;  NUMBER OF SEQ ID NOS: 21
 ;  SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 8
 ;   LENGTH: 42
 ;   TYPE: DNA
 ;   ORGANISM: Homo sapiens
US-09-590-211A-8

  Query Match             1.8%;  Score 28.8;  DB 22;  Length 42;
  Best Local Similarity   82.5%;  Pred. No. 5e+05;
  Matches   33;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   1346 GGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCA 1385
           || | | |||||||||| | | |||| ||||||||||||
Db      3 GGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCA 42


RESULT 6
PCT-US02-26129-14
; Sequence 14, Application PC/TUS0226129
; GENERAL INFORMATION:
 ;  APPLICANT: OriGene Technologies
 ;  APPLICANT:  OriGene Technologies
 ;  TITLE OF INVENTION: Serine Protein Kinase in Brain and Pancreas
 ;  FILE REFERENCE: 16U 101 PCT
 ;  CURRENT APPLICATION NUMBER: PCT/US02/26129
 ;  CURRENT FILING DATE:  2002-08-16
 ;  PRIOR APPLICATION NUMBER: US 09/930,181
 ;  PRIOR FILING DATE: 2001-08-16
 ;  NUMBER OF SEQ ID NOS: 18
 ;  SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 14
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-26129-14

  Query Match             1.8%;  Score 28.2;  DB 1;  Length 50;
  Best Local Similarity   73.5%;  Pred. No. 6.2e+05;
  Matches   36;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy   1336 GGACCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGC 1384
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Db      1 GGCGCGGGGCGCGGGCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGAAGC 49


RESULT 7
US-10-195-071-14
; Sequence 14, Application US/10195071
; GENERAL INFORMATION:
;  APPLICANT: OriGene Technologies
;  TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
;  FILE REFERENCE: 16U 101 C1
;  CURRENT APPLICATION NUMBER: US/10/195,071
;  CURRENT FILING DATE:  2002-07-15
;  PRIOR APPLICATION NUMBER: US 09/930,181
;  PRIOR FILING DATE: 2001-08-16
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-195-071-14

  Query Match             1.8%;  Score 28.2;  DB 41;  Length 50;
  Best Local Similarity   73.5%;  Pred. No. 6.2e+05;
  Matches   36;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy   1336 GGACCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGC 1384
          ||  || |||| || |  ||||||||| | | |||| ||||||||  ||
Db      1 GGCGCGGGGCGCGGGCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGAAGC 49


RESULT 8
US-10-195-072-14
; Sequence 14, Application US/10195072
; GENERAL INFORMATION:
;  APPLICANT: OriGene Technologies
;  TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
;  FILE REFERENCE: 16U 101 C2
;  CURRENT APPLICATION NUMBER: US/10/195,072
;  CURRENT FILING DATE:  2002-07-15
;  PRIOR APPLICATION NUMBER: US 09/930,181
;  PRIOR FILING DATE: 2001-08-16
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-195-072-14

  Query Match             1.8%;  Score 28.2;  DB 41;  Length 50;
  Best Local Similarity   73.5%;  Pred. No. 6.2e+05;
  Matches   36;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy   1336 GGACCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGC 1384
          ||  || |||| || |  ||||||||| | | |||| ||||||||  ||
Db      1 GGCGCGGGGCGCGGGCCTCGGCGGCGGCGGCGGCGGCGGCGGCGGAAGC 49


RESULT 9
US-09-590-211-7
; Sequence 7, Application US/09590211
; GENERAL INFORMATION:
;  APPLICANT: Rouleau, Guy A.
;  APPLICANT:  Brais, Bernard
;  TITLE OF INVENTION: Short GCG Expansions in the PAB II Gene
;  TITLE OF INVENTION:  for Oculopharyngeal Muscular Dystrophy and Diagnostic
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: 3028.1000-000
;  CURRENT APPLICATION NUMBER: US/09/590,211
;  CURRENT FILING DATE:  2000-06-08
;  PRIOR APPLICATION NUMBER: PCT/CA98/01133
;  PRIOR FILING DATE: 1998-12-07
;  PRIOR APPLICATION NUMBER: 2,218,199
;  PRIOR FILING DATE: 1997-12-09
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 39
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-590-211-7

  Query Match             1.7%;  Score 27.4;  DB 22;  Length 39;
  Best Local Similarity   83.8%;  Pred. No. 8.4e+05;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   1349 GACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCA 1385
          | | |||||||||| | | |||| ||||||||||||
Db      3 GGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCA 39


RESULT 10
US-09-590-211A-7
; Sequence 7, Application US/09590211A
; GENERAL INFORMATION:
;  APPLICANT: Rouleau, Guy A.
;  APPLICANT:  Brais, Bernard
;  TITLE OF INVENTION: SHORT GCG EXPANSIONS IN THE PAB II GENE
;  TITLE OF INVENTION:  FOR OCULOPHARYNGEAL MUSCULAR DYSTROPHY AND DIAGNOSTIC THere
;  FILE REFERENCE: 3028.1000-000
;  CURRENT APPLICATION NUMBER: US/09/590,211A
;  CURRENT FILING DATE:  2000-06-08
;  PRIOR APPLICATION NUMBER: PCT/CA98/01133
;  PRIOR FILING DATE: 1998-12-07
;  PRIOR APPLICATION NUMBER: 2,218,199
;  PRIOR FILING DATE: 1997-12-09
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 39
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-590-211A-7

  Query Match             1.7%;  Score 27.4;  DB 22;  Length 39;
  Best Local Similarity   83.8%;  Pred. No. 8.4e+05;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   1349 GACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCA 1385
          | | |||||||||| | | |||| ||||||||||||
Db      3 GGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCA 39


RESULT 11
US-09-992-665-289/c
; Sequence 289, Application US/09992665
; GENERAL INFORMATION:
;  APPLICANT: Kaia Palm
;  TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
;  TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
;  FILE REFERENCE: CEMINES.002A
;  CURRENT APPLICATION NUMBER: US/09/992,665
;  CURRENT FILING DATE:  2001-11-13
```

```
;  PRIOR APPLICATION NUMBER: 60/249,508
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 380
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 289
;    LENGTH: 27
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Probe
US-09-992-665-289

  Query Match             1.7%;  Score 27;  DB 37;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     755 TCGGCCACGGTGCACCTGGAGCAGGGC 781
           |||||||||||||||||||||||||||
Db      27 TCGGCCACGGTGCACCTGGAGCAGGGC 1


RESULT 12
US-09-590-211-6
; Sequence 6, Application US/09590211
; GENERAL INFORMATION:
;  APPLICANT: Rouleau, Guy A.
;  APPLICANT:  Brais, Bernard
;  TITLE OF INVENTION: Short GCG Expansions in the PAB II Gene
;  TITLE OF INVENTION:  for Oculopharyngeal Muscular Dystrophy and Diagnostic
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: 3028.1000-000
;  CURRENT APPLICATION NUMBER: US/09/590,211
;  CURRENT FILING DATE:  2000-06-08
;  PRIOR APPLICATION NUMBER: PCT/CA98/01133
;  PRIOR FILING DATE: 1998-12-07
;  PRIOR APPLICATION NUMBER: 2,218,199
;  PRIOR FILING DATE: 1997-12-09
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;    LENGTH: 36
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-590-211-6

  Query Match             1.7%;  Score 26.6;  DB 22;  Length 36;
  Best Local Similarity   87.9%;  Pred. No. 1.1e+06;
  Matches   29;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    1353 GCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCA 1385
           |||||||||| | | |||| ||||||||||||
Db       4 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCA 36


RESULT 13
US-09-590-211A-6
; Sequence 6, Application US/09590211A
; GENERAL INFORMATION:
;  APPLICANT: Rouleau, Guy A.
;  APPLICANT:  Brais, Bernard
;  TITLE OF INVENTION: SHORT GCG EXPANSIONS IN THE PAB II GENE
;  TITLE OF INVENTION:  FOR OCULOPHARYNGEAL MUSCULAR DYSTROPHY AND DIAGNOSTIC THereof
;  FILE REFERENCE: 3028.1000-000
;  CURRENT APPLICATION NUMBER: US/09/590,211A
;  CURRENT FILING DATE:  2000-06-08
;  PRIOR APPLICATION NUMBER: PCT/CA98/01133
;  PRIOR FILING DATE: 1998-12-07
;  PRIOR APPLICATION NUMBER: 2,218,199
;  PRIOR FILING DATE: 1997-12-09
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;    LENGTH: 36
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-590-211A-6

  Query Match             1.7%;  Score 26.6;  DB 22;  Length 36;
  Best Local Similarity   87.9%;  Pred. No. 1.1e+06;
  Matches   29;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    1353 GCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCA 1385
           |||||||||| | | |||| ||||||||||||
Db       4 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCA 36


RESULT 14
US-09-423-041A-2/c
; Sequence 2, Application US/09423041A
; GENERAL INFORMATION:
;  APPLICANT: Cassandra L. Smith
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETED
;  TITLE OF INVENTION:  DNA DIFFERENTIAL DISPLAY
;  FILE REFERENCE: BU-042XX
;  CURRENT APPLICATION NUMBER: US/09/423,041A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: PCT/US98/08616
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: US60/045,078
;  PRIOR FILING DATE: 1997-04-29
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;    LENGTH: 36
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Probe/Primer
US-09-423-041A-2

  Query Match             1.7%;  Score 26.4;  DB 18;  Length 36;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+06;
  Matches   30;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    1351 CAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCAG 1386
           | |||||||||| | | |||| |||||||||||| |
Db      36 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1


RESULT 15
PCT-US00-19843-13
; Sequence 13, Application PC/TUS0019843
; GENERAL INFORMATION:
;  APPLICANT:  Herr, John C.                                          ;
;  APPLICANT:  Norton, Elizabeth J.
;  APPLICANT:  Deikman, Alan B.
;  TITLE OF INVENTION:  Recombinant Antibody Directed Against Human Sperm
;  TITLE OF INVENTION:  Antigen
;  FILE REFERENCE:  00415-02
;  CURRENT APPLICATION NUMBER: PCT/US00/19843
;  CURRENT FILING DATE:  2000-07-21
;  PRIOR APPLICATION NUMBER:  60/145,512
;  PRIOR FILING DATE:  1999-07-23
;  NUMBER OF SEQ ID NOS:  18
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 13
;    LENGTH: 45
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
;    OTHER INFORMATION: linker
PCT-US00-19843-13

  Query Match             1.7%;  Score 26.4;  DB 1;  Length 45;
  Best Local Similarity   75.0%;  Pred. No. 1.2e+06;
```

```
  Matches   33;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   1341 GCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGC 1384
          ||||||| | |||||| || || |     ||||||||||| ||
Db      2 GCGGCGGCGGCAGCGGTGGTGGTGGTTCTGGGGGCGGCGGCAGC 45


RESULT 16
US-10-031-783-13
; Sequence 13, Application US/10031783
; GENERAL INFORMATION:
;  APPLICANT: Herr, John C.
;  APPLICANT:  Norton, Elizabeth J.
;  APPLICANT:  Deikman, Alan B.
;  TITLE OF INVENTION: Recombinant Antibody Directed Against Human Sperm
;  TITLE OF INVENTION:  Antigen
;  FILE REFERENCE: 00415-02
;  CURRENT APPLICATION NUMBER: US/10/031,783
;  CURRENT FILING DATE:  2002-10-23
;  PRIOR APPLICATION NUMBER: 60/145,512
;  PRIOR FILING DATE: 1999-07-23
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 45
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
;   OTHER INFORMATION: linker
US-10-031-783-13

  Query Match             1.7%;  Score 26.4;  DB 38;  Length 45;
  Best Local Similarity   75.0%;  Pred. No. 1.2e+06;
  Matches   33;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   1341 GCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGC 1384
          ||||||| | |||||| || || |     ||||||||||| ||
Db      2 GCGGCGGCGGCAGCGGTGGTGGTGGTTCTGGGGGCGGCGGCAGC 45


RESULT 17
US-09-606-755-17709
; Sequence 17709, Application US/09606755
; GENERAL INFORMATION:
;  APPLICANT: Havukkala, Ilkka
;  APPLICANT:  Shenk, Michael A.
;  TITLE OF INVENTION: Polynucleotides, Materials Incorporating
;  TITLE OF INVENTION:  Them, and Methods for Using Them
;  FILE REFERENCE: 11000.1041U6
;  CURRENT APPLICATION NUMBER: US/09/606,755
;  CURRENT FILING DATE:  2000-06-22
;  NUMBER OF SEQ ID NOS: 17747
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17709
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Pinus radiata
US-09-606-755-17709

  Query Match             1.6%;  Score 26;  DB 23;  Length 50;
  Best Local Similarity   70.0%;  Pred. No. 1.4e+06;
  Matches   35;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     19 GAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGA 68
          ||||||| ||| | | |||   ||| |||  || || || |  |||||||
Db      1 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 50


RESULT 18
US-09-857-723-178/c
; Sequence 178, Application US/09857723
; GENERAL INFORMATION:
;  APPLICANT: Alcivar-Warren, Acacia
;  APPLICANT:  Xu, Zhenkang
;  APPLICANT:  Dhar, Arun K.
;  APPLICANT:  Fan, Yongjun
;  APPLICANT:  Meehan, Dawn
;  APPLICANT:  Garcia, Denise K.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES OF SHRIMP
;  FILE REFERENCE: 1322.1023-003
;  CURRENT APPLICATION NUMBER: US/09/857,723
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/111,670
;  PRIOR FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 292
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Litopenaeus vannamei
;   FEATURE:
;   NAME/KEY: satellite
;   LOCATION: (1)...(50)
US-09-857-723-178

  Query Match             1.6%;  Score 26;  DB 32;  Length 50;
  Best Local Similarity   70.0%;  Pred. No. 1.4e+06;
  Matches   35;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     19 GAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGA 68
          ||||||| ||| | | |||   ||| |||  || || || |  |||||||
Db     50 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 1


RESULT 19
US-09-857-723-187/c
; Sequence 187, Application US/09857723
; GENERAL INFORMATION:
;  APPLICANT: Alcivar-Warren, Acacia
;  APPLICANT:  Xu, Zhenkang
;  APPLICANT:  Dhar, Arun K.
;  APPLICANT:  Fan, Yongjun
;  APPLICANT:  Meehan, Dawn
;  APPLICANT:  Garcia, Denise K.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES OF SHRIMP
;  FILE REFERENCE: 1322.1023-003
;  CURRENT APPLICATION NUMBER: US/09/857,723
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/111,670
;  PRIOR FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 292
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 187
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Litopenaeus vannamei
;   FEATURE:
;   NAME/KEY: satellite
;   LOCATION: (1)...(50)
US-09-857-723-187

  Query Match             1.6%;  Score 26;  DB 32;  Length 50;
  Best Local Similarity   70.0%;  Pred. No. 1.4e+06;
  Matches   35;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     20 AGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGAG 69
          |||||| ||| | | |||   ||| |||  || || || |  ||||||||
Db     50 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1


RESULT 20
US-09-857-723-199/c
; Sequence 199, Application US/09857723
; GENERAL INFORMATION:
;  APPLICANT: Alcivar-Warren, Acacia
```

```
 ;  APPLICANT:  Xu, Zhenkang
 ;  APPLICANT:  Dhar, Arun K.
 ;  APPLICANT:  Fan, Yongjun
 ;  APPLICANT:  Meehan, Dawn
 ;  APPLICANT:  Garcia, Denise K.
 ;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES OF SHRIMP
 ;  FILE REFERENCE: 1322.1023-003
 ;  CURRENT APPLICATION NUMBER: US/09/857,723
 ;  CURRENT FILING DATE:  2001-06-07
 ;  PRIOR APPLICATION NUMBER: 60/111,670
 ;  PRIOR FILING DATE: 1998-12-10
 ;  NUMBER OF SEQ ID NOS: 292
 ;  SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 199
 ;    LENGTH: 50
 ;    TYPE: DNA
 ;    ORGANISM: Litopenaeus vannamei
 ;    FEATURE:
 ;    NAME/KEY: satellite
 ;    LOCATION: (1)...(50)
US-09-857-723-199

  Query Match             1.6%;  Score 26;  DB 32;  Length 50;
  Best Local Similarity   70.0%;  Pred. No. 1.4e+06;
  Matches   35;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy      19 GAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGA 68
           ||||||| ||| | | |||   ||| |||  || || || |  |||||||
Db      50 GAGAGAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 1


RESULT 21
US-08-715-713-17
; Sequence 17, Application US/08715713
;  GENERAL INFORMATION:
;    APPLICANT:  Innis, Jeffrey W.
;    APPLICANT:  Mortlock, Douglas P.
;    APPLICANT:  Nelson, Matt
;    TITLE OF INVENTION:  PROMOTER CAPTURE
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montomgery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/715,713
;      FILING DATE:  19-SEP-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carroll, Peter G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  UM-02402
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "DNA"
US-08-715-713-17

  Query Match             1.6%;  Score 25.6;  DB 11;  Length 50;
  Best Local Similarity   77.5%;  Pred. No. 1.6e+06;
  Matches   31;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy    1337 GACCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCG 1376
           |||  |||||| | ||||||||||||   | |||| ||||
Db      11 GACAACGGCGGCGGCAGCGGCGGCGGCCGCGGCGGCGGCG 50


RESULT 22
US-09-396-196F-67173
; Sequence 67173, Application US/09396196F
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196F
;  CURRENT FILING DATE:  2001-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67173
;    LENGTH: 25
;    TYPE: DNA
;    ORGANISM: mus musculus
US-09-396-196F-67173

  Query Match             1.6%;  Score 25;  DB 17;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1443 GCATCCACTGGTACTCGCAGCTGCT 1467
           |||||||||||||||||||||||||
Db       1 GCATCCACTGGTACTCGCAGCTGCT 25


RESULT 23
US-09-396-196F-67174
; Sequence 67174, Application US/09396196F
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196F
;  CURRENT FILING DATE:  2001-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67174
;    LENGTH: 25
;    TYPE: DNA
;    ORGANISM: mus musculus
US-09-396-196F-67174

  Query Match             1.6%;  Score 25;  DB 17;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1446 TCCACTGGTACTCGCAGCTGCTCTA 1470
           |||||||||||||||||||||||||
Db       1 TCCACTGGTACTCGCAGCTGCTCTA 25


RESULT 24
US-09-396-196F-67183
```

```
; Sequence 67183, Application US/09396196F
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196F
;  CURRENT FILING DATE:  2001-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67183
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196F-67183

  Query Match             1.6%;  Score 25;  DB 17;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1206 GCACCATTCTCATCAACCGGGTGCT 1230
          |||||||||||||||||||||||||
Db      1 GCACCATTCTCATCAACCGGGTGCT 25


RESULT 25
US-09-396-196G-67173
; Sequence 67173, Application US/09396196G
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67173
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-67173

  Query Match             1.6%;  Score 25;  DB 17;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+06;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1443 GCATCCACTGGTACTCGCAGCTGCT 1467
          |||||||||||||||||||||||||
Db      1 GCATCCACTGGTACTCGCAGCTGCT 25


Search completed: March 14, 2003, 01:02:17
Job time : 3791 secs
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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 13, 2003, 21:59:18 ; Search time 476 Seconds
(without alignments)
7520.095 Million cell updates/sec

Title: US-10-001-844-3
Perfect score: 1576
Sequence: 1 gcgaggcagccagcgaggga.....gaggggcgcgggaggggggcc 1576

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4665808 seqs, 1135648920 residues

Total number of hits satisfying chosen parameters: 7025612

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2:*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
9: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	30	1.9	30	8	US-10-001-844-6	Sequence 6, Appli
	2	26.4	1.7	44	7	US-10-287-787-7843	Sequence 7843, Ap
c	3	26	1.6	46	7	US-10-299-054A-10448	Sequence 10448, A
	4	25.6	1.6	43	7	US-10-299-054A-10430	Sequence 10430, A
	5	25.6	1.6	43	7	US-10-299-054A-10431	Sequence 10431, A
	6	25.6	1.6	43	7	US-10-299-054A-10449	Sequence 10449, A
	7	25.6	1.6	43	7	US-10-299-054A-10450	Sequence 10450, A
c	8	25.6	1.6	50	8	US-10-126-448-2	Sequence 2, Appli
c	9	25	1.6	25	8	US-10-303-778-10110	Sequence 10110, A
	10	25	1.6	25	9	US-60-427-808-296803	Sequence 296803,
	11	25	1.6	25	9	US-60-427-808-634065	Sequence 634065,
	12	25	1.6	25	9	US-60-427-836-454485	Sequence 454485,
	13	25	1.6	50	6	US-09-912-293-16672	Sequence 16672, A
	14	24.4	1.5	50	8	US-10-351-951-54	Sequence 54, Appl
	15	24	1.5	24	6	US-09-711-724A-43	Sequence 43, Appl
	16	23.4	1.5	25	9	US-60-427-808-121712	Sequence 121712,
	17	23.4	1.5	25	9	US-60-427-808-296804	Sequence 296804,
	18	23.4	1.5	25	9	US-60-427-808-634064	Sequence 634064,
	19	23.4	1.5	25	9	US-60-427-808-765746	Sequence 765746,
	20	23.4	1.5	25	9	US-60-427-808-807373	Sequence 807373,
	21	23.4	1.5	25	9	US-60-427-808-879497	Sequence 879497,
	22	23.4	1.5	25	9	US-60-427-836-90500	Sequence 90500, A
	23	23.4	1.5	25	9	US-60-427-836-238304	Sequence 238304,
	24	23.4	1.5	25	9	US-60-427-836-454484	Sequence 454484,
	25	23.4	1.5	25	9	US-60-427-836-591791	Sequence 591791,
c	26	23.4	1.5	42	7	US-10-299-054A-7072	Sequence 7072, Ap
	27	23.4	1.5	42	7	US-10-299-054A-8125	Sequence 8125, Ap
	28	23.4	1.5	48	7	US-10-299-054A-6989	Sequence 6989, Ap
c	29	23	1.5	49	7	US-10-299-054A-2490	Sequence 2490, Ap
	30	23	1.5	50	1	PCT-US03-02612-18	Sequence 18, Appl
	31	23	1.5	50	1	PCT-US03-02612-96	Sequence 96, Appl
	32	22.8	1.4	41	7	US-10-287-787-12533	Sequence 12533, A
	33	22.8	1.4	45	7	US-10-299-054A-10693	Sequence 10693, A
	34	22.8	1.4	48	7	US-10-299-054A-10634	Sequence 10634, A
c	35	22.8	1.4	50	7	US-10-299-054A-7061	Sequence 7061, Ap
	36	22.6	1.4	30	8	US-10-281-513-332	Sequence 332, App
	37	22.6	1.4	45	7	US-10-299-054A-9407	Sequence 9407, Ap
	38	22.6	1.4	46	7	US-10-299-054A-3300	Sequence 3300, Ap
c	39	22.6	1.4	50	6	US-09-513-999C-30835	Sequence 30835, A
	40	22.6	1.4	50	6	US-09-912-293-18324	Sequence 18324, A
c	41	22.6	1.4	50	6	US-09-912-293-104036	Sequence 104036,
	42	22.4	1.4	25	9	US-60-427-808-825912	Sequence 825912,
	43	22.4	1.4	40	7	US-10-299-054A-10610	Sequence 10610, A
c	44	22.4	1.4	40	7	US-10-299-054A-10611	Sequence 10611, A
	45	22.4	1.4	40	7	US-10-299-054A-10612	Sequence 10612, A
	46	22.4	1.4	40	7	US-10-299-054A-10613	Sequence 10613, A
c	47	22.4	1.4	40	7	US-10-299-054A-10614	Sequence 10614, A
	48	22.4	1.4	40	7	US-10-299-054A-10615	Sequence 10615, A
c	49	22.4	1.4	50	7	US-10-299-054A-10467	Sequence 10467, A
	50	22.2	1.4	39	6	US-09-548-797B-146	Sequence 146, App
	51	22.2	1.4	41	8	US-10-277-216-383	Sequence 383, App
c	52	22.2	1.4	50	9	US-60-288-292-9341	Sequence 9341, Ap
c	53	22	1.4	29	8	US-10-164-282-19	Sequence 19, Appl
	54	22	1.4	39	7	US-10-299-054A-1613	Sequence 1613, Ap
	55	22	1.4	39	7	US-10-299-054A-9444	Sequence 9444, Ap
	56	21.8	1.4	25	9	US-60-427-808-121711	Sequence 121711,
	57	21.8	1.4	25	9	US-60-427-808-765747	Sequence 765747,
	58	21.8	1.4	25	9	US-60-427-808-807374	Sequence 807374,
	59	21.8	1.4	25	9	US-60-427-808-823929	Sequence 823929,
	60	21.8	1.4	25	9	US-60-427-808-879498	Sequence 879498,
	61	21.8	1.4	25	9	US-60-427-836-90499	Sequence 90499, A
	62	21.8	1.4	25	9	US-60-427-836-238305	Sequence 238305,
	63	21.8	1.4	25	9	US-60-427-836-591790	Sequence 591790,
c	64	21.8	1.4	41	7	US-10-299-054A-9492	Sequence 9492, Ap
	65	21.8	1.4	41	7	US-10-299-054A-10705	Sequence 10705, A
c	66	21.8	1.4	41	7	US-10-299-054A-10706	Sequence 10706, A
c	67	21.8	1.4	41	7	US-10-299-054A-10708	Sequence 10708, A
c	68	21.8	1.4	42	7	US-10-299-054A-1211	Sequence 1211, Ap
	69	21.8	1.4	43	7	US-10-299-054A-9427	Sequence 9427, Ap
	70	21.8	1.4	50	7	US-10-299-054A-9464	Sequence 9464, Ap
	71	21.6	1.4	43	7	US-10-367-892-12230	Sequence 12230, A
c	72	21.6	1.4	46	7	US-10-299-054A-6233	Sequence 6233, Ap
c	73	21.6	1.4	46	9	US-60-288-292-11658	Sequence 11658, A
c	74	21.6	1.4	50	7	US-10-287-787-7195	Sequence 7195, Ap
	75	21.4	1.4	41	7	US-10-299-054A-10665	Sequence 10665, A
	76	21.4	1.4	41	7	US-10-299-054A-10666	Sequence 10666, A
	77	21.4	1.4	42	8	US-10-224-661A-14	Sequence 14, Appl
	78	21.4	1.4	45	8	US-10-015-610A-151	Sequence 151, App
	79	21.4	1.4	45	8	US-10-226-254A-151	Sequence 151, App
	80	21.4	1.4	45	8	US-10-017-253A-151	Sequence 151, App
	81	21.4	1.4	50	6	US-09-912-293-18701	Sequence 18701, A
	82	21.4	1.4	50	6	US-09-912-293-67589	Sequence 67589, A
	83	21.2	1.3	42	7	US-10-299-054A-197	Sequence 197, App
c	84	21.2	1.3	43	7	US-10-299-054A-7349	Sequence 7349, Ap
c	85	21.2	1.3	43	7	US-10-299-054A-8103	Sequence 8103, Ap
c	86	21.2	1.3	44	7	US-10-299-054A-3265	Sequence 3265, Ap
c	87	21.2	1.3	44	7	US-10-299-054A-4273	Sequence 4273, Ap
	88	21.2	1.3	47	7	US-10-287-787-4906	Sequence 4906, Ap
c	89	21.2	1.3	50	6	US-09-912-293-164157	Sequence 164157,
c	90	21	1.3	21	8	US-10-310-188-64439	Sequence 64439, A
	91	21	1.3	21	8	US-10-001-844-4	Sequence 4, Appli
	92	21	1.3	42	7	US-10-299-054A-723	Sequence 723, App
c	93	21	1.3	50	8	US-10-329-624-2153	Sequence 2153, Ap
	94	20.8	1.3	25	9	US-60-427-808-825913	Sequence 825913,
c	95	20.8	1.3	25	9	US-60-427-836-654494	Sequence 654494,
c	96	20.8	1.3	32	7	US-10-299-054A-10607	Sequence 10607, A
c	97	20.8	1.3	40	7	US-10-367-892-7237	Sequence 7237, Ap

c 98	20.8	1.3	42	7	US-10-299-054A-4333	Sequence 4333, Ap
99	20.8	1.3	46	7	US-10-299-054A-7060	Sequence 7060, Ap
c 100	20.8	1.3	46	7	US-10-287-787-9487	Sequence 9487, Ap
c 101	20.8	1.3	48	7	US-10-299-054A-10445	Sequence 10445, A
c 102	20.8	1.3	48	7	US-10-299-054A-10464	Sequence 10464, A
c 103	20.8	1.3	48	8	US-10-187-394-33	Sequence 33, Appl
c 104	20.8	1.3	50	7	US-10-287-787-9699	Sequence 9699, Ap
105	20.8	1.3	50	7	US-10-287-787-26352	Sequence 26352, A
106	20.6	1.3	38	7	US-10-299-054A-1159	Sequence 1159, Ap
107	20.6	1.3	39	6	US-09-548-797B-145	Sequence 145, App
c 108	20.6	1.3	40	7	US-10-367-892-20998	Sequence 20998, A
109	20.6	1.3	41	8	US-10-277-216-251	Sequence 251, App
c 110	20.6	1.3	45	7	US-10-299-054A-9465	Sequence 9465, Ap
c 111	20.6	1.3	50	6	US-09-912-293-133717	Sequence 133717,
112	20.6	1.3	50	6	US-09-912-293-230617	Sequence 230617,
c 113	20.4	1.3	30	8	US-10-314-578-1096	Sequence 1096, Ap
114	20.4	1.3	31	7	US-10-299-054A-10609	Sequence 10609, A
c 115	20.4	1.3	32	7	US-10-367-892-4004	Sequence 4004, Ap
c 116	20.4	1.3	35	6	US-09-888-326A-172	Sequence 172, App
c 117	20.4	1.3	35	8	US-10-314-578-771	Sequence 771, App
118	20.4	1.3	38	7	US-10-299-054A-2212	Sequence 2212, Ap
119	20.4	1.3	38	7	US-10-287-787-22474	Sequence 22474, A
120	20.4	1.3	39	7	US-10-299-054A-10598	Sequence 10598, A
c 121	20.4	1.3	40	7	US-10-299-054A-9406	Sequence 9406, Ap
c 122	20.4	1.3	40	7	US-10-287-787-4905	Sequence 4905, Ap
123	20.4	1.3	41	7	US-10-367-892-14922	Sequence 14922, A
c 124	20.4	1.3	42	8	US-10-224-661A-15	Sequence 15, Appl
c 125	20.4	1.3	44	7	US-10-287-787-12769	Sequence 12769, A
c 126	20.4	1.3	45	7	US-10-367-892-12335	Sequence 12335, A
127	20.4	1.3	46	7	US-10-299-054A-9746	Sequence 9746, Ap
128	20.4	1.3	48	7	US-10-367-892-11618	Sequence 11618, A
129	20.4	1.3	50	6	US-09-912-293-67368	Sequence 67368, A
c 130	20.4	1.3	50	7	US-10-299-054A-10599	Sequence 10599, A
131	20.4	1.3	50	8	US-10-329-624-5127	Sequence 5127, Ap
132	20.2	1.3	25	9	US-60-427-808-823928	Sequence 823928,
133	20.2	1.3	25	9	US-60-427-836-590247	Sequence 590247,
134	20.2	1.3	30	7	US-10-287-787-23287	Sequence 23287, A
c 135	20.2	1.3	33	7	US-10-287-787-16472	Sequence 16472, A
c 136	20.2	1.3	40	9	US-60-416-172-117	Sequence 117, App
137	20.2	1.3	41	7	US-10-299-054A-2492	Sequence 2492, Ap
138	20.2	1.3	41	7	US-10-287-787-1598	Sequence 1598, Ap
c 139	20.2	1.3	41	7	US-10-287-787-23892	Sequence 23892, A
140	20.2	1.3	42	7	US-10-299-054A-2491	Sequence 2491, Ap
c 141	20.2	1.3	43	7	US-10-299-054A-3309	Sequence 3309, Ap
c 142	20.2	1.3	45	7	US-10-367-892-22163	Sequence 22163, A
143	20.2	1.3	45	7	US-10-299-054A-6232	Sequence 6232, Ap
c 144	20.2	1.3	45	7	US-10-299-054A-10719	Sequence 10719, A
145	20.2	1.3	50	7	US-10-299-054A-10698	Sequence 10698, A
c 146	20	1.3	20	8	US-10-001-844-10	Sequence 10, Appl
c 147	20	1.3	20	8	US-10-001-844-11	Sequence 11, Appl
c 148	20	1.3	20	8	US-10-001-844-12	Sequence 12, Appl
c 149	20	1.3	20	8	US-10-001-844-13	Sequence 13, Appl
c 150	20	1.3	20	8	US-10-001-844-14	Sequence 14, Appl
c 151	20	1.3	20	8	US-10-001-844-15	Sequence 15, Appl
c 152	20	1.3	20	8	US-10-001-844-16	Sequence 16, Appl
c 153	20	1.3	20	8	US-10-001-844-17	Sequence 17, Appl
c 154	20	1.3	20	8	US-10-001-844-18	Sequence 18, Appl
c 155	20	1.3	20	8	US-10-001-844-19	Sequence 19, Appl
c 156	20	1.3	20	8	US-10-001-844-20	Sequence 20, Appl
c 157	20	1.3	20	8	US-10-001-844-21	Sequence 21, Appl
c 158	20	1.3	20	8	US-10-001-844-22	Sequence 22, Appl
c 159	20	1.3	20	8	US-10-001-844-23	Sequence 23, Appl
c 160	20	1.3	20	8	US-10-001-844-24	Sequence 24, Appl
c 161	20	1.3	20	8	US-10-001-844-25	Sequence 25, Appl
c 162	20	1.3	20	8	US-10-001-844-26	Sequence 26, Appl
c 163	20	1.3	20	8	US-10-001-844-27	Sequence 27, Appl
c 164	20	1.3	20	8	US-10-001-844-28	Sequence 28, Appl
c 165	20	1.3	20	8	US-10-001-844-29	Sequence 29, Appl
c 166	20	1.3	20	8	US-10-001-844-30	Sequence 30, Appl
c 167	20	1.3	20	8	US-10-001-844-31	Sequence 31, Appl
c 168	20	1.3	20	8	US-10-001-844-32	Sequence 32, Appl
c 169	20	1.3	20	8	US-10-001-844-33	Sequence 33, Appl
c 170	20	1.3	20	8	US-10-001-844-34	Sequence 34, Appl
c 171	20	1.3	20	8	US-10-001-844-35	Sequence 35, Appl
c 172	20	1.3	20	8	US-10-001-844-36	Sequence 36, Appl
c 173	20	1.3	20	8	US-10-001-844-37	Sequence 37, Appl
c 174	20	1.3	20	8	US-10-001-844-38	Sequence 38, Appl
c 175	20	1.3	20	8	US-10-001-844-39	Sequence 39, Appl
c 176	20	1.3	20	8	US-10-001-844-40	Sequence 40, Appl
c 177	20	1.3	20	8	US-10-001-844-41	Sequence 41, Appl
c 178	20	1.3	20	8	US-10-001-844-42	Sequence 42, Appl
c 179	20	1.3	20	8	US-10-001-844-43	Sequence 43, Appl
c 180	20	1.3	20	8	US-10-001-844-44	Sequence 44, Appl
c 181	20	1.3	20	8	US-10-001-844-45	Sequence 45, Appl
c 182	20	1.3	20	8	US-10-001-844-46	Sequence 46, Appl
c 183	20	1.3	20	8	US-10-001-844-47	Sequence 47, Appl
c 184	20	1.3	20	8	US-10-001-844-48	Sequence 48, Appl
c 185	20	1.3	20	8	US-10-001-844-49	Sequence 49, Appl
186	20	1.3	31	7	US-10-299-054A-2219	Sequence 2219, Ap
187	20	1.3	36	7	US-10-367-892-8624	Sequence 8624, Ap
188	20	1.3	36	8	US-10-332-542-15	Sequence 15, Appl
c 189	20	1.3	38	7	US-10-367-892-6205	Sequence 6205, Ap
c 190	20	1.3	38	7	US-10-367-892-14921	Sequence 14921, A
191	20	1.3	40	7	US-10-287-787-5968	Sequence 5968, Ap
192	20	1.3	45	6	US-09-989-733-122	Sequence 122, App
193	20	1.3	45	6	US-09-992-643-122	Sequence 122, App
194	20	1.3	45	7	US-10-299-054A-8129	Sequence 8129, Ap
c 195	20	1.3	47	6	US-09-785-632B-6	Sequence 6, Appli
c 196	20	1.3	47	7	US-10-299-054A-9753	Sequence 9753, Ap
197	20	1.3	50	6	US-09-912-293-231186	Sequence 231186,
198	19.8	1.3	24	8	US-10-310-188-74357	Sequence 74357, A
199	19.8	1.3	31	7	US-10-299-054A-10608	Sequence 10608, A
200	19.8	1.3	39	7	US-10-287-787-13541	Sequence 13541, A
201	19.8	1.3	40	7	US-10-299-054A-9491	Sequence 9491, Ap
202	19.8	1.3	41	7	US-10-299-054A-9410	Sequence 9410, Ap
203	19.8	1.3	43	7	US-10-299-054A-3149	Sequence 3149, Ap
204	19.8	1.3	44	6	US-09-705-552A-1	Sequence 1, Appli
205	19.8	1.3	48	9	US-60-288-292-32448	Sequence 32448, A
c 206	19.8	1.3	50	6	US-09-912-293-48904	Sequence 48904, A
207	19.8	1.3	50	7	US-10-367-892-9874	Sequence 9874, Ap
208	19.6	1.2	27	8	US-10-310-188-48780	Sequence 48780, A
209	19.6	1.2	34	7	US-10-299-054A-10854	Sequence 10854, A
c 210	19.6	1.2	41	7	US-10-367-892-12752	Sequence 12752, A
211	19.6	1.2	43	7	US-10-299-054A-1327	Sequence 1327, Ap
212	19.6	1.2	44	7	US-10-367-892-12751	Sequence 12751, A
213	19.6	1.2	44	7	US-10-299-054A-4273	Sequence 4273, Ap
214	19.6	1.2	44	8	US-10-316-956-1844	Sequence 1844, Ap
215	19.6	1.2	46	5	US-09-762-862-8	Sequence 8, Appli
216	19.6	1.2	46	5	US-09-762-867A-8	Sequence 8, Appli
217	19.6	1.2	46	7	US-10-762-862-8	Sequence 8, Appli
218	19.6	1.2	50	6	US-09-912-293-18731	Sequence 18731, A
c 219	19.6	1.2	50	6	US-09-912-293-205920	Sequence 205920,
220	19.6	1.2	50	7	US-10-287-787-21723	Sequence 21723, A
c 221	19.6	1.2	50	8	US-10-325-899-181	Sequence 181, App
222	19.4	1.2	21	8	US-10-303-778-11706	Sequence 11706, A
c 223	19.4	1.2	32	7	US-10-299-054A-7050	Sequence 7050, Ap
224	19.4	1.2	38	1	PCT-US02-38288-185	Sequence 185, App
c 225	19.4	1.2	38	7	US-10-299-054A-5405	Sequence 5405, Ap
226	19.4	1.2	38	7	US-10-299-054A-5406	Sequence 5406, Ap
c 227	19.4	1.2	38	7	US-10-299-054A-5407	Sequence 5407, Ap
228	19.4	1.2	38	7	US-10-299-054A-10600	Sequence 10600, A
229	19.4	1.2	38	8	US-10-308-128-185	Sequence 185, App
230	19.4	1.2	43	7	US-10-367-892-11707	Sequence 11707, A
c 231	19.4	1.2	45	7	US-10-367-892-25167	Sequence 25167, A
c 232	19.4	1.2	45	7	US-10-287-787-22294	Sequence 22294, A
c 233	19.4	1.2	46	7	US-10-299-054A-3826	Sequence 3826, Ap
c 234	19.4	1.2	46	7	US-10-299-054A-10674	Sequence 10674, A
c 235	19.4	1.2	46	7	US-10-287-787-13357	Sequence 13357, A
c 236	19.4	1.2	47	7	US-10-287-787-405	Sequence 405, App
237	19.4	1.2	47	8	US-10-349-143-2037	Sequence 2037, Ap
238	19.4	1.2	47	8	US-10-349-143-2552	Sequence 2552, Ap
c 239	19.4	1.2	49	7	US-10-299-054A-10530	Sequence 10530, A
240	19.4	1.2	49	7	US-10-287-787-20144	Sequence 20144, A
241	19.4	1.2	50	6	US-09-765-555A-25	Sequence 25, Appl
c 242	19.4	1.2	50	6	US-09-912-293-171148	Sequence 171148,
243	19.4	1.2	50	7	US-10-299-054A-8379	Sequence 8379, Ap

	244	19.4	1.2	50	7	US-10-287-787-8559
	245	19.4	1.2	50	8	US-10-325-899-523
	246	19.2	1.2	24	8	US-10-310-188-48644
	247	19.2	1.2	24	8	US-10-310-188-48659
	248	19.2	1.2	25	8	US-10-355-577-63773
	249	19.2	1.2	25	9	US-60-427-808-83180
c	250	19.2	1.2	25	9	US-60-427-836-225534
c	251	19.2	1.2	25	9	US-60-427-836-244066
	252	19.2	1.2	25	9	US-60-427-836-385452
c	253	19.2	1.2	25	9	US-60-427-836-654493
c	254	19.2	1.2	32	8	US-10-270-524-20
c	255	19.2	1.2	33	7	US-10-299-054A-10857
	256	19.2	1.2	34	7	US-10-299-054A-3310
c	257	19.2	1.2	34	7	US-10-287-787-16578
	258	19.2	1.2	38	7	US-10-367-892-12802
c	259	19.2	1.2	38	7	US-10-299-054A-7692
	260	19.2	1.2	38	7	US-10-299-054A-10622
c	261	19.2	1.2	39	7	US-10-299-054A-3972
	262	19.2	1.2	39	7	US-10-299-054A-7337
c	263	19.2	1.2	40	7	US-10-367-892-9687
c	264	19.2	1.2	40	7	US-10-287-787-11738
	265	19.2	1.2	40	7	US-10-287-787-16577
	266	19.2	1.2	41	7	US-10-287-787-13882
c	267	19.2	1.2	41	8	US-10-310-157-2531
	268	19.2	1.2	42	7	US-10-299-054A-10675
c	269	19.2	1.2	42	8	US-10-211-088-100
	270	19.2	1.2	44	8	US-10-316-956-236
c	271	19.2	1.2	45	7	US-10-367-892-21770
	272	19.2	1.2	46	7	US-10-287-787-12519
	273	19.2	1.2	47	7	US-10-299-054A-2372
c	274	19.2	1.2	48	7	US-10-299-054A-9829
	275	19.2	1.2	48	7	US-10-299-054A-9830
c	276	19.2	1.2	48	7	US-10-299-054A-9831
c	277	19.2	1.2	48	7	US-10-287-787-11584
	278	19.2	1.2	49	7	US-10-367-892-20906
	279	19.2	1.2	50	6	US-09-912-293-234351
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	281	19.2	1.2	50	8	US-10-325-899-3427
	282	19	1.2	19	6	US-09-825-155A-5
	283	19	1.2	19	6	US-09-825-155A-9
c	284	19	1.2	19	8	US-10-303-778-3424
c	285	19	1.2	19	8	US-10-310-188-5772
	286	19	1.2	19	8	US-10-310-188-60793
c	287	19	1.2	29	7	US-10-299-054A-7038
	288	19	1.2	30	7	US-10-367-892-11708
	289	19	1.2	30	8	US-10-164-282-18
	290	19	1.2	33	7	US-10-299-054A-740
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	292	19	1.2	38	7	US-10-299-054A-2610
	293	19	1.2	38	7	US-10-299-054A-10480
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	295	19	1.2	39	7	US-10-299-054A-9732
	296	19	1.2	39	7	US-10-299-054A-10479
	297	19	1.2	39	8	US-10-343-561-141
	298	19	1.2	40	1	PCT-US02-26708-53
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	304	19	1.2	40	8	US-10-224-683-53
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c	308	19	1.2	41	8	US-10-008-960-32
	309	19	1.2	42	7	US-10-367-892-6782
	310	19	1.2	43	7	US-10-299-054A-1757
	311	19	1.2	43	7	US-10-299-054A-3333
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	313	19	1.2	44	7	US-10-287-787-6829
	314	19	1.2	45	7	US-10-367-892-8798
	315	19	1.2	45	7	US-10-299-054A-329
	316	19	1.2	45	7	US-10-299-054A-4381

Sequence 8559, Ap
Sequence 523, App
Sequence 48644, A
Sequence 48659, A
Sequence 63773, A
Sequence 83180, A
Sequence 225534,
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Sequence 385452,
Sequence 654493,
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Sequence 5, Appli
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	319	19	1.2	45	8	US-10-089-058A-60
	320	19	1.2	47	6	US-09-785-632B-7
	321	19	1.2	47	7	US-10-299-054A-10800
	322	19	1.2	47	7	US-10-299-054A-10806
	323	19	1.2	48	6	US-09-708-506A-16
	324	19	1.2	48	7	US-10-367-892-25020
c	325	19	1.2	49	7	US-10-287-787-22173
c	326	19	1.2	50	8	US-10-325-899-4902
	327	18.8	1.2	22	8	US-10-310-188-29562
	328	18.8	1.2	25	9	US-60-427-836-346047
	329	18.8	1.2	25	9	US-60-427-836-654281
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	331	18.8	1.2	32	7	US-10-299-054A-5501
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	333	18.8	1.2	33	7	US-10-299-054A-5500
	334	18.8	1.2	37	7	US-10-299-054A-3266
	335	18.8	1.2	38	7	US-10-299-054A-5201
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c	337	18.8	1.2	39	7	US-10-299-054A-11189
	338	18.8	1.2	39	8	US-10-305-275-1473
	339	18.8	1.2	39	8	US-10-305-275A-1473
	340	18.8	1.2	40	6	US-09-875-082-75
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c	348	18.8	1.2	42	1	PCT-US02-41414-946
	349	18.8	1.2	42	8	US-10-132-295-4
	350	18.8	1.2	42	8	US-10-209-208-65
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	352	18.8	1.2	43	9	US-60-288-292-7836
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	354	18.8	1.2	45	7	US-10-299-054A-5505
	355	18.8	1.2	46	7	US-10-299-054A-3271
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	357	18.8	1.2	46	7	US-10-299-054A-4356
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	359	18.8	1.2	46	7	US-10-287-787-13357
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	367	18.8	1.2	49	7	US-10-287-787-4251
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	371	18.8	1.2	50	8	US-10-325-899-4569
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	379	18.6	1.2	25	9	US-60-427-808-304565
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	381	18.6	1.2	25	9	US-60-427-808-623289
	382	18.6	1.2	25	9	US-60-427-808-872100
	383	18.6	1.2	25	9	US-60-427-808-876926
	384	18.6	1.2	25	9	US-60-427-836-81274
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	386	18.6	1.2	25	9	US-60-427-836-398939
	387	18.6	1.2	25	9	US-60-427-836-590246
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Sequence 5126, Ap
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Sequence 7, Appli
Sequence 10800, A
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Sequence 56, Appl
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Sequence 15, Appl

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	403	18.6	1.2	41	1	PCT-US02-35375-33
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	405	18.6	1.2	41	7	US-10-299-054A-2224
	406	18.6	1.2	41	8	US-10-319-369-2
	407	18.6	1.2	42	7	US-10-299-054A-2494
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c	410	18.6	1.2	42	7	US-10-287-787-24733
c	411	18.6	1.2	43	7	US-10-367-892-17749
	412	18.6	1.2	43	7	US-10-367-892-25041
	413	18.6	1.2	43	7	US-10-287-787-21378
c	414	18.6	1.2	44	7	US-10-299-054A-6131
	415	18.6	1.2	44	7	US-10-299-054A-11059
c	416	18.6	1.2	44	7	US-10-287-787-6829
	417	18.6	1.2	44	8	US-10-316-956-256
	418	18.6	1.2	45	6	US-09-906-777B-313
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	421	18.6	1.2	45	6	US-09-904-011C-313
	422	18.6	1.2	45	6	US-09-665-350B-313
	423	18.6	1.2	45	7	US-10-287-787-1205
	424	18.6	1.2	45	8	US-10-299-937-313
	425	18.6	1.2	45	8	US-10-299-976-313
	426	18.6	1.2	45	8	US-10-298-993-313
	427	18.6	1.2	46	7	US-10-299-054A-6233
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	433	18.6	1.2	49	7	US-10-299-054A-11058
c	434	18.6	1.2	49	8	US-10-083-246A-56
c	435	18.6	1.2	50	6	US-09-912-293-62813
	436	18.6	1.2	50	7	US-10-299-054A-2880
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c	447	18.4	1.2	29	8	US-10-228-264-17
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	453	18.4	1.2	32	7	US-10-299-054A-601
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	457	18.4	1.2	36	8	US-10-332-542-7
c	458	18.4	1.2	37	7	US-10-299-054A-8130
	459	18.4	1.2	37	7	US-10-299-054A-11191
	460	18.4	1.2	37	7	US-10-287-787-27647
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Sequence 7, Appli
Sequence 12768, A
Sequence 9417, Ap
Sequence 10505, A
Sequence 10532, A
Sequence 5419, Ap
Sequence 5418, Ap
Sequence 2223, Ap
Sequence 5416, Ap
Sequence 5417, Ap
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Sequence 313, App
Sequence 122, App
Sequence 122, App
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Sequence 56, Appl
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Sequence 171, App
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Sequence 16, Appl
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Sequence 17084, A
Sequence 17434, A
Sequence 601, App
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Sequence 27647, A
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Sequence 2240, Ap

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	466	18.4	1.2	44	7	US-10-299-054A-9578
	467	18.4	1.2	44	7	US-10-299-054A-9679
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c	469	18.4	1.2	44	7	US-10-299-054A-10684
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	472	18.4	1.2	46	6	US-09-770-169A-76
c	473	18.4	1.2	47	7	US-10-299-054A-8046
	474	18.4	1.2	47	7	US-10-299-054A-11262
c	475	18.4	1.2	47	7	US-10-287-787-4527
c	476	18.4	1.2	48	7	US-10-367-892-6684
	477	18.4	1.2	48	7	US-10-367-892-17619
	478	18.4	1.2	49	6	US-09-785-632B-8
c	479	18.4	1.2	49	7	US-10-299-054A-6930
c	480	18.4	1.2	50	6	US-09-912-293-120093
	481	18.4	1.2	50	6	US-09-912-293-229061
	482	18.4	1.2	50	7	US-10-287-787-11402
c	483	18.4	1.2	50	8	US-10-325-899-451
	484	18.4	1.2	50	8	US-10-325-899-6536
	485	18.4	1.2	50	8	US-10-325-899-6599
c	486	18.4	1.2	50	8	US-10-325-899-6926
c	487	18.4	1.2	50	8	US-10-325-899-6989
	488	18.4	1.2	50	8	US-10-325-899-7175
	489	18.2	1.2	23	8	US-10-310-188-35370
	490	18.2	1.2	24	8	US-10-310-188-67051
	491	18.2	1.2	24	8	US-10-310-188-74369
c	492	18.2	1.2	25	7	US-10-299-054A-7009
	493	18.2	1.2	25	7	US-10-299-054A-7010
c	494	18.2	1.2	25	8	US-10-355-577-340709
	495	18.2	1.2	25	8	US-10-355-577-363921
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	497	18.2	1.2	25	8	US-10-355-577-594243
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	499	18.2	1.2	25	9	US-60-427-808-191387
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	501	18.2	1.2	25	9	US-60-427-808-926319
	502	18.2	1.2	25	9	US-60-427-836-391325
	503	18.2	1.2	31	6	US-09-911-935C-10
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Sequence 13729, A
Sequence 2527, Ap
Sequence 10683, A
Sequence 9578, Ap
Sequence 9679, Ap
Sequence 9680, Ap
Sequence 10684, A
Sequence 34, Appl
Sequence 6232, Ap
Sequence 76, Appl
Sequence 8046, Ap
Sequence 11262, A
Sequence 4527, Ap
Sequence 6684, Ap
Sequence 17619, A
Sequence 8, Appli
Sequence 6930, Ap
Sequence 120093,
Sequence 229061,
Sequence 11402, A
Sequence 451, App
Sequence 6536, Ap
Sequence 6599, Ap
Sequence 6926, Ap
Sequence 6989, Ap
Sequence 7175, Ap
Sequence 35370, A
Sequence 67051, A
Sequence 74369, A
Sequence 7009, Ap
Sequence 7010, Ap
Sequence 340709,
Sequence 363921,
Sequence 479181,
Sequence 594243,
Sequence 594244,
Sequence 191387,
Sequence 248076,
Sequence 926319,
Sequence 391325,
Sequence 10, Appl
Sequence 16471, A
Sequence 25466, A
Sequence 24507, A
Sequence 9502, Ap
Sequence 14920, A
Sequence 748, App
Sequence 9445, Ap
Sequence 8431, Ap
Sequence 19553, A
Sequence 21667, A
Sequence 16344, A
Sequence 11966, A
Sequence 6130, Ap
Sequence 7441, Ap
Sequence 9443, Ap
Sequence 1473, Ap
Sequence 1473, Ap
Sequence 2495, Ap
Sequence 3169, Ap
Sequence 12650, A
Sequence 418, App
Sequence 647, App
Sequence 817, App
Sequence 13408, A
Sequence 24081, A
Sequence 34, Appl
Sequence 20803, A
Sequence 4173, Ap
Sequence 9674, Ap
Sequence 10448, A
Sequence 19048, A
Sequence 6995, Ap

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Sequence 16985, A
Sequence 20906, A
Sequence 10438, A
Sequence 10458, A
Sequence 41502, A
Sequence 43353, A
Sequence 210464,
Sequence 75, Appl
Sequence 3908, Ap
Sequence 6766, Ap
Sequence 7156, Ap
Sequence 7341, Ap
Sequence 7450, Ap
Sequence 7529, Ap
Sequence 6, Appli
Sequence 39805, A
Sequence 42147, A
Sequence 20, Appl
Sequence 21, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 9430, Ap
Sequence 10312, A
Sequence 18, Appl
Sequence 22, Appl
Sequence 37, Appl
Sequence 24522, A
Sequence 10365, A
Sequence 10366, A
Sequence 10743, A
Sequence 10744, A
Sequence 3680, Ap
Sequence 7043, Ap
Sequence 9207, Ap
Sequence 28, Appl
Sequence 101, App
Sequence 1336, Ap
Sequence 1117, Ap
Sequence 1117, Ap
Sequence 5928, Ap
Sequence 2531, Ap
Sequence 17, Appl
Sequence 540, App
Sequence 7066, Ap
Sequence 7067, Ap
Sequence 320, App
Sequence 100, App
Sequence 9575, Ap
Sequence 25747, A
Sequence 20, Appl
Sequence 855, App
Sequence 26840, A
Sequence 441, App
Sequence 10379, A
Sequence 10755, A
Sequence 8, Appli
Sequence 6031, Ap
Sequence 10308, A
Sequence 17473, A
Sequence 8, Appli
Sequence 15747, A
Sequence 2081, Ap
Sequence 22, Appl
Sequence 29, Appl
Sequence 15934, A
Sequence 14644, A
Sequence 16488, A
Sequence 22, Appl
Sequence 53, Appl
Sequence 7604, Ap
Sequence 5445, Ap
Sequence 9291, Ap
Sequence 174987,

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Sequence 206403,
Sequence 15511, A
Sequence 3253, Ap
Sequence 4175, Ap
Sequence 10525, A
Sequence 10526, A
Sequence 7195, Ap
Sequence 26952, A
Sequence 181, App
Sequence 191, App
Sequence 613, App
Sequence 1877, Ap
Sequence 2047, Ap
Sequence 7338, Ap
Sequence 7579, Ap
Sequence 181, App
Sequence 9815, Ap
Sequence 48653, A
Sequence 70629, A
Sequence 29666, A
Sequence 48703, A
Sequence 753758,
Sequence 455510,
Sequence 302171,
Sequence 353357,
Sequence 560494,
Sequence 2510, Ap
Sequence 11394, A
Sequence 3343, Ap
Sequence 3344, Ap
Sequence 23005, A
Sequence 51809, A
Sequence 19, Appl
Sequence 22622, A
Sequence 2237, Ap
Sequence 2498, Ap
Sequence 2499, Ap
Sequence 2192, Ap
Sequence 2475, Ap
Sequence 2476, Ap
Sequence 5473, Ap
Sequence 24709, A
Sequence 250, App
Sequence 9853, Ap
Sequence 2191, Ap
Sequence 6990, Ap
Sequence 12, Appl
Sequence 3736, Ap
Sequence 1703, Ap
Sequence 30, Appl
Sequence 12, Appl
Sequence 2944, Ap
Sequence 3972, Ap
Sequence 10508, A
Sequence 16040, A
Sequence 835, App
Sequence 37, Appl
Sequence 47, Appl
Sequence 16002, A
Sequence 37, Appl
Sequence 1287, Ap
Sequence 653, App
Sequence 2200, Ap
Sequence 2235, Ap
Sequence 2236, Ap
Sequence 5472, Ap
Sequence 24733, A
Sequence 18853, A
Sequence 10430, A
Sequence 10431, A
Sequence 10449, A
Sequence 10450, A
Sequence 22145, A

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	773	17.6	1.1	32	7	US-10-299-054A-8451 Sequence 8451, Ap
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	784	17.6	1.1	35	7	US-10-299-054A-715 Sequence 715, App
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	787	17.6	1.1	36	8	US-10-008-960-28 Sequence 28, Appl
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Sequence 14, Appl
Sequence 3822, Ap
Sequence 439, App
Sequence 2533, Ap
Sequence 151340,
Sequence 206403,
Sequence 10698, A
Sequence 64402, A
Sequence 72649, A
Sequence 7246, Ap
Sequence 61175, A
Sequence 254344,
Sequence 451372,
Sequence 1, Appli
Sequence 3145, Ap
Sequence 70548, A
Sequence 15477, A
Sequence 4, Appli
Sequence 10847, A
Sequence 7887, Ap
Sequence 19371, A
Sequence 229, App
Sequence 3820, Ap
Sequence 189, App
Sequence 1589, Ap
Sequence 14270, A
Sequence 11833, A
Sequence 12520, A
Sequence 11625, A
Sequence 2204, Ap
Sequence 11146, A
Sequence 8, Appli
Sequence 1750, Ap
Sequence 67, Appl
Sequence 15, Appl
Sequence 9484, Ap
Sequence 9456, Ap
Sequence 1573, Ap
Sequence 15753, A
Sequence 10064, A
Sequence 10196, A
Sequence 11915, A
Sequence 14761, A
Sequence 18576, A
Sequence 765, App
Sequence 15381, A
Sequence 546, App
Sequence 169, App
Sequence 23519, A
Sequence 62, Appl
Sequence 19240, A
Sequence 241, App
Sequence 266, App
Sequence 62, Appl
Sequence 756, App
Sequence 22, Appl
Sequence 7790, Ap
Sequence 9471, Ap
Sequence 10819, A
Sequence 14, Appl
Sequence 22, Appl
Sequence 240, App
Sequence 10829, A
Sequence 10829, A
Sequence 6423, Ap
Sequence 26798, A
Sequence 9234, Ap
Sequence 1392, Ap
Sequence 10820, A
Sequence 10821, A
Sequence 10833, A
Sequence 10834, A
Sequence 10835, A

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	968	17.2	1.1	25	9	US-60-427-808-665304
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c	971	17.2	1.1	25	9	US-60-427-836-247311
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Sequence 10846, A
Sequence 10848, A
Sequence 19197, A
Sequence 3283, Ap
Sequence 9593, Ap
Sequence 20535, A
Sequence 25024, A
Sequence 15747, A
Sequence 2372, Ap
Sequence 8046, Ap
Sequence 9816, Ap
Sequence 6060, Ap
Sequence 7518, Ap
Sequence 18121, A
Sequence 24713, A
Sequence 3847, Ap
Sequence 10, Appl
Sequence 16488, A
Sequence 26979, A
Sequence 8, Appli
Sequence 19414, A
Sequence 15423, A
Sequence 15638, A
Sequence 23, Appl
Sequence 117, App
Sequence 49078, A
Sequence 85925, A
Sequence 9707, Ap
Sequence 32, Appl
Sequence 33, Appl
Sequence 1357, Ap
Sequence 2488, Ap
Sequence 3562, Ap
Sequence 3779, Ap
Sequence 6258, Ap
Sequence 29465, A
Sequence 58413, A
Sequence 60588, A
Sequence 60894, A
Sequence 29478, A
Sequence 49888, A
Sequence 12, Appl
Sequence 6811, Ap
Sequence 17317, A
Sequence 15480, A
Sequence 29553, A
Sequence 41628, A
Sequence 70671, A
Sequence 12, Appl
Sequence 21387, A
Sequence 118079,
Sequence 123028,
Sequence 136971,
Sequence 114707,
Sequence 361802,
Sequence 574883,
Sequence 601568,
Sequence 618769,
Sequence 683836,
Sequence 120038,
Sequence 120039,
Sequence 120045,
Sequence 120046,
Sequence 164185,
Sequence 323982,
Sequence 323983,
Sequence 392595,
Sequence 665304,
Sequence 181306,
Sequence 184860,
Sequence 247311,
Sequence 289180,
Sequence 346045,

974	17.2	1.1	25	9	US-60-427-836-399282	Sequence 399282,
c 975	17.2	1.1	25	9	US-60-427-836-652973	Sequence 652973,
976	17.2	1.1	25	9	US-60-427-836-653150	Sequence 653150,
977	17.2	1.1	25	9	US-60-427-836-654282	Sequence 654282,
978	17.2	1.1	25	9	US-60-427-836-663449	Sequence 663449,
c 979	17.2	1.1	30	7	US-10-367-892-21796	Sequence 21796, A
980	17.2	1.1	30	7	US-10-299-054A-608	Sequence 608, App
c 981	17.2	1.1	30	7	US-10-299-054A-649	Sequence 649, App
982	17.2	1.1	30	7	US-10-299-054A-4199	Sequence 4199, Ap
983	17.2	1.1	30	7	US-10-299-054A-8978	Sequence 8978, Ap
c 984	17.2	1.1	30	7	US-10-299-054A-10856	Sequence 10856, A
985	17.2	1.1	30	7	US-10-287-787-12674	Sequence 12674, A
c 986	17.2	1.1	30	7	US-10-287-787-14195	Sequence 14195, A
987	17.2	1.1	30	7	US-10-287-787-14822	Sequence 14822, A
988	17.2	1.1	30	7	US-10-287-787-16473	Sequence 16473, A
c 989	17.2	1.1	30	8	US-10-316-954-4456	Sequence 4456, Ap
990	17.2	1.1	30	8	US-10-314-578-1097	Sequence 1097, Ap
c 991	17.2	1.1	30	8	US-10-314-578-1097	Sequence 1097, Ap
c 992	17.2	1.1	31	7	US-10-367-892-7821	Sequence 7821, Ap
993	17.2	1.1	31	7	US-10-299-054A-3456	Sequence 3456, Ap
994	17.2	1.1	32	7	US-10-367-892-4362	Sequence 4362, Ap
c 995	17.2	1.1	32	7	US-10-287-787-13994	Sequence 13994, A
c 996	17.2	1.1	33	1	PCT-US02-24274-11	Sequence 11, Appl
997	17.2	1.1	33	7	US-10-287-787-19712	Sequence 19712, A
998	17.2	1.1	34	7	US-10-287-787-10660	Sequence 10660, A
c 999	17.2	1.1	35	7	US-10-367-892-964	Sequence 964, App
1000	17.2	1.1	37	7	US-10-287-787-8179	Sequence 8179, Ap

ALIGNMENTS

```
RESULT 1
US-10-001-844-6
; Sequence 6, Application US/10001844
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
;  FILE REFERENCE: ISPH-0617
;  CURRENT APPLICATION NUMBER: US/10/001,844
;  CURRENT FILING DATE:  2001-11-16
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR Probe
US-10-001-844-6

  Query Match             1.9%;  Score 30;  DB 8;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     691 TATCCACTGCTCGGTGAAAGCAGAGAACTC 720
           ||||||||||||||||||||||||||||||
Db       1 TATCCACTGCTCGGTGAAAGCAGAGAACTC 30


RESULT 2
US-10-287-787-7843
; Sequence 7843, Application US/10287787
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Caulobacter crescentus complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/287,787
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 27958
;  SOFTWARE: Proprietary
; SEQ ID NO 7843
;   LENGTH: 44
;   TYPE: DNA
;   ORGANISM: Caulobacter crescentus complete genome.
;   FEATURE:
;   LOCATION: (1052967)...(1053010)
;   OTHER INFORMATION: Chromosome = 1  Strand = positive  ConnectronObjectNumber =
US-10-287-787-7843

  Query Match             1.7%;  Score 26.4;  DB 7;  Length 44;
  Best Local Similarity   75.0%;  Pred. No. 5.9e+04;
  Matches   33;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    1351 CAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCAGAGTAGCCC 1394
           | ||| ||||| ||||| ||| |||||||||| ||   | | ||
Db       1 CTGCGCCGGCGCGGACCTCGGCGGCGGCGGCGCCACCTTCGACC 44


RESULT 3
US-10-299-054A-10448/c
; Sequence 10448, Application US/10299054A
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/299,054A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 11910
;  SOFTWARE: Proprietary
; SEQ ID NO 10448
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis complete genome.
;   FEATURE:
;   LOCATION: (3933994)...(3934039)
;   OTHER INFORMATION: Chromosome = 1  Strand = negative  ConnectronObjectNumber = 1
US-10-299-054A-10448

  Query Match             1.6%;  Score 26;  DB 7;  Length 46;
  Best Local Similarity   76.2%;  Pred. No. 7e+04;
  Matches   32;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    1337 GACCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGC 1378
           | |||||||||| ||| |||||| |||| | ||||   ||||
Db      45 GGCCGCGGCGGTGACGGCGGCGATGGGGCCAGCGGTCTCGGC 4


RESULT 4
US-10-299-054A-10430
; Sequence 10430, Application US/10299054A
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/299,054A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 11910
;  SOFTWARE: Proprietary
; SEQ ID NO 10430
;   LENGTH: 43
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis complete genome.
;   FEATURE:
;   LOCATION: (3933394)...(3933436)
;   OTHER INFORMATION: Chromosome = 1  Strand = positive  ConnectronObjectNumber =
US-10-299-054A-10430

  Query Match             1.6%;  Score 25.6;  DB 7;  Length 43;
  Best Local Similarity   77.5%;  Pred. No. 8.1e+04;
  Matches   31;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy    1339 CCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGC 1378
           ||||||||| ||| |||||| |||| | ||||   ||||
Db       1 CCGCGGCGGTGACGGCGGCGATGGGGCCAGCGGTCTCGGC 40
```

```
RESULT 5
US-10-299-054A-10431
; Sequence 10431, Application US/10299054A
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/299,054A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 11910
;  SOFTWARE: Proprietary
; SEQ ID NO 10431
;    LENGTH: 43
;    TYPE: DNA
;    ORGANISM: Mycobacterium tuberculosis complete genome.
;    FEATURE:
;    LOCATION: (3933394)...(3933436)
;    OTHER INFORMATION: Chromosome = 1  Strand = positive  ConnectronObjectNumber = 12507
US-10-299-054A-10431

  Query Match             1.6%;  Score 25.6;  DB 7;  Length 43;
  Best Local Similarity   77.5%;  Pred. No. 8.1e+04;
  Matches   31;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   1339 CCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGC 1378
           ||||||||| ||| ||||||  |||| | ||||   ||||
Db      1 CCGCGGCGGTGACGGCGGCGATGGGGCCAGCGGTCTCGGC 40


RESULT 6
US-10-299-054A-10449
; Sequence 10449, Application US/10299054A
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/299,054A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 11910
;  SOFTWARE: Proprietary
; SEQ ID NO 10449
;    LENGTH: 43
;    TYPE: DNA
;    ORGANISM: Mycobacterium tuberculosis complete genome.
;    FEATURE:
;    LOCATION: (3933997)...(3934039)
;    OTHER INFORMATION: Chromosome = 1  Strand = positive  ConnectronObjectNumber = 12527
US-10-299-054A-10449

  Query Match             1.6%;  Score 25.6;  DB 7;  Length 43;
  Best Local Similarity   77.5%;  Pred. No. 8.1e+04;
  Matches   31;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   1339 CCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGC 1378
           ||||||||| ||| ||||||  |||| | ||||   ||||
Db      1 CCGCGGCGGTGACGGCGGCGATGGGGCCAGCGGTCTCGGC 40


RESULT 7
US-10-299-054A-10450
; Sequence 10450, Application US/10299054A
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/299,054A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 11910
;  SOFTWARE: Proprietary
; SEQ ID NO 10450
;    LENGTH: 43
;    TYPE: DNA
;    ORGANISM: Mycobacterium tuberculosis complete genome.
;    FEATURE:
;    LOCATION: (3933997)...(3934039)
;    OTHER INFORMATION: Chromosome = 1  Strand = positive  ConnectronObjectNumber =
US-10-299-054A-10450

  Query Match             1.6%;  Score 25.6;  DB 7;  Length 43;
  Best Local Similarity   77.5%;  Pred. No. 8.1e+04;
  Matches   31;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   1339 CCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGC 1378
           ||||||||| ||| ||||||  |||| | ||||   ||||
Db      1 CCGCGGCGGTGACGGCGGCGATGGGGCCAGCGGTCTCGGC 40


RESULT 8
US-10-126-448-2/c
; Sequence 2, Application US/10126448
; GENERAL INFORMATION:
;  APPLICANT: Doring, Volker
;  APPLICANT:  Nangle, Leslie A.
;  APPLICANT:  Hendrickson, Tamara L.
;  APPLICANT:  de Crecy-Lagard, Valerie
;  APPLICANT:  Schimmel, Paul
;  APPLICANT:  Marliere, Philippe
;  TITLE OF INVENTION: Method for Diversifying the Chemical
;  TITLE OF INVENTION:  Composition of Proteins Produced in vivo by Genetically
;  TITLE OF INVENTION:  Disabling the Editing Function of their Aminoacyl tRNA
;  TITLE OF INVENTION:  Synthetases
;  FILE REFERENCE: CABI-004
;  CURRENT APPLICATION NUMBER: US/10/126,448
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: US 60/285,495
;  PRIOR FILING DATE: 2001-04-19
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;    LENGTH: 50
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: synthetic oligonucleotide
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: 1
;    OTHER INFORMATION: N = phosphorylated cytidine
US-10-126-448-2

  Query Match             1.6%;  Score 25.6;  DB 8;  Length 50;
  Best Local Similarity   87.5%;  Pred. No. 8.2e+04;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1353 GCGGCGGCGGGGACCGCGGGGGCGGCGGCGGC 1384
           |||||||||| | | |||| ||||||||||||
Db     45 GCGGCGGCGGCGGCGGCGGCGGCGGCGGC 14


RESULT 9
US-10-303-778-10110/c
; Sequence 10110, Application US/10303778
; GENERAL INFORMATION:
;  APPLICANT: RosettaGenomics
;  TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
;  TITLE OF INVENTION:  REGULATORY GENES AND USES THEREOF
;  FILE REFERENCE: 47416
;  CURRENT APPLICATION NUMBER: US/10/303,778
;  CURRENT FILING DATE:  2002-11-26
;  NUMBER OF SEQ ID NOS: 17608
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10110
;    LENGTH: 25
;    TYPE: DNA
```

```
;   ORGANISM: Homo sapiens
US-10-303-778-10110

  Query Match             1.6%;  Score 25;  DB 8;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.8e+04;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1551 CCGGGGGAGGGGCGCGGGAGGGGGC 1575
           |||||||||||||||||||||||||
Db      25 CCGGGGGAGGGGCGCGGGAGGGGGC 1


RESULT 10
US-60-427-808-296803
; Sequence 296803, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 296803
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-296803

  Query Match             1.6%;  Score 25;  DB 9;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.8e+04;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     895 CAAGAAGGTCTTCTACGTGATCGAG 919
           |||||||||||||||||||||||||
Db       1 CAAGAAGGTCTTCTACGTGATCGAG 25


RESULT 11
US-60-427-808-634065
; Sequence 634065, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 634065
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-634065

  Query Match             1.6%;  Score 25;  DB 9;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.8e+04;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1441 GGGCATCCACTGGTACTCGCAGCTG 1465
           |||||||||||||||||||||||||
Db       1 GGGCATCCACTGGTACTCGCAGCTG 25


RESULT 12
US-60-427-836-454485
; Sequence 454485, Application US/60427836
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527
;  CURRENT APPLICATION NUMBER: US/60/427,836
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 454485
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-60-427-836-454485

  Query Match             1.6%;  Score 25;  DB 9;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.8e+04;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1441 GGGCATCCACTGGTACTCGCAGCTG 1465
           |||||||||||||||||||||||||
Db       1 GGGCATCCACTGGTACTCGCAGCTG 25


RESULT 13
US-09-912-293-16672
; Sequence 16672, Application US/09912293
; GENERAL INFORMATION:
;  APPLICANT: Rosen, et. al.
;  TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
;  FILE REFERENCE: PO-100
;  CURRENT APPLICATION NUMBER: US/09/912,293
;  CURRENT FILING DATE:  2001-07-26
;  PRIOR APPLICATION NUMBER: 08/103,744
;  PRIOR FILING DATE: 1993-08-09
;  PRIOR APPLICATION NUMBER: 09/249,651
;  PRIOR FILING DATE: 1999-02-12
;  PRIOR APPLICATION NUMBER: 08/104,507
;  PRIOR FILING DATE: 1993-08-09
;  PRIOR APPLICATION NUMBER: 08/196,363
;  PRIOR FILING DATE: 1994-02-15
;  PRIOR APPLICATION NUMBER: 09/859,490
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: 08/196,362
;  PRIOR FILING DATE: 1994-02-15
;  PRIOR APPLICATION NUMBER: 08/221,623
;  PRIOR FILING DATE: 1994-03-31
;  PRIOR APPLICATION NUMBER: 08/220,691
;  PRIOR FILING DATE: 1994-03-31
;  PRIOR APPLICATION NUMBER: 09/741,830
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 09/813,155
;  PRIOR FILING DATE: 2001-03-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 244538
; SEQ ID NO 16672
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (50)..(50)
;   OTHER INFORMATION: n is equal to a,t,g, or c
US-09-912-293-16672

  Query Match             1.6%;  Score 25;  DB 6;  Length 50;
  Best Local Similarity   69.4%;  Pred. No. 1e+05;
  Matches   34;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       5 GGCAGCCAGCGAGGGAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGG 53
           |||||  || ||| ||||||| ||| | | |||   ||| |||  || |
Db       1 GGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 49


RESULT 14
US-10-351-951-54
; Sequence 54, Application US/10351951
; GENERAL INFORMATION:
;  APPLICANT: Stefansson, Stefan E.
;  TITLE OF INVENTION: GENE LINKED TO OSTEOARTHRITIS
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```
;  FILE REFERENCE: 2345.2043-004
;  CURRENT APPLICATION NUMBER: US/10/351,951
;  CURRENT FILING DATE:  2003-01-24
;  PRIOR APPLICATION NUMBER: 10/057,312
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: 60/431,538
;  PRIOR FILING DATE: 2002-12-05
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-351-951-54

  Query Match             1.5%;  Score 24.4;  DB 8;  Length 50;
  Best Local Similarity   68.0%;  Pred. No. 1.3e+05;
  Matches   34;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   1310 CTGGCTGCACTGGCGCCCGCGCGCACGGACCGCGGCGGGGACAGCGGCGG 1359
          | ||| |  ||||||| || |  | |||  || ||||||| | | ||| |
Db      1 CGGGCCGGCCTGGCGCTCGAGGCCCCGGGGCGGGGCGGGGCCCGAGGCCG 50


RESULT 15
US-09-711-724A-43
; Sequence 43, Application US/09711724A
; GENERAL INFORMATION:
;  APPLICANT: Ingham et al.
;  TITLE OF INVENTION: SCREENING ASSAYS FOR HEDGEHOG AGONISTS AND ANTAGONISTS
;  FILE REFERENCE: HMSU-P14-006
;  CURRENT APPLICATION NUMBER: US/09/711,724A
;  CURRENT FILING DATE:  2000-11-13
;  PRIOR APPLICATION NUMBER: 08/674509
;  PRIOR FILING DATE: 1996-07-07
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-09-711-724A-43

  Query Match             1.5%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    524 ACCGAGGGCTGGGACGAAGATGGC 547
          ||||||||||||||||||||||||
Db      1 ACCGAGGGCTGGGACGAAGATGGC 24


RESULT 16
US-60-427-808-121712
; Sequence 121712, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 121712
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-121712

  Query Match             1.5%;  Score 23.4;  DB 9;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 1.8e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1203 AGGGCACCATTCTCATCAACCGGGT 1227
          | |||||||||||||||||||||||
Db      1 ACGGCACCATTCTCATCAACCGGGT 25


RESULT 17
US-60-427-808-296804
; Sequence 296804, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 296804
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-296804

  Query Match             1.5%;  Score 23.4;  DB 9;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 1.8e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    895 CAAGAAGGTCTTCTACGTGATCGAG 919
          ||||||||||||| |||||||||||||
Db      1 CAAGAAGGTCTTGTACGTGATCGAG 25


RESULT 18
US-60-427-808-634064
; Sequence 634064, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 634064
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-634064

  Query Match             1.5%;  Score 23.4;  DB 9;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 1.8e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1441 GGGCATCCACTGGTACTCGCAGCTG 1465
          |||||||||||| ||||||||||||
Db      1 GGGCATCCACTGCTACTCGCAGCTG 25


RESULT 19
US-60-427-808-765746
; Sequence 765746, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 765746
;   LENGTH: 25
;   TYPE: DNA
```

```
;   ORGANISM: Mus musculus
US-60-427-808-765746

  Query Match              1.5%;  Score 23.4;  DB 9;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 1.8e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     908 TACGTGATCGAGACGCGGGAGCCGC 932
           ||||||||||||||| ||||||||
Db       1 TACGTGATCGAGACGCTGGAGCCGC 25


RESULT 20
US-60-427-808-807373
; Sequence 807373, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 807373
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-807373

  Query Match              1.5%;  Score 23.4;  DB 9;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 1.8e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1248 TCATCGAGGAGCACAGCTGGGCGCA 1272
           ||||||||||||||||||||||| ||
Db       1 TCATCGAGGAGCACAGCTGGGCACA 25


RESULT 21
US-60-427-808-879497
; Sequence 879497, Application US/60427808
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528
;  CURRENT APPLICATION NUMBER: US/60/427,808
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 879497
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-60-427-808-879497

  Query Match              1.5%;  Score 23.4;  DB 9;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 1.8e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     876 TGGACCGCGACGACGGCGCCAAGAA 900
           ||||||||||||| ||||||||||
Db       1 TGGACCGCGACGAAGGCGCCAAGAA 25


RESULT 22
US-60-427-836-90500
; Sequence 90500, Application US/60427836
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527
;  CURRENT APPLICATION NUMBER: US/60/427,836
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90500
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-60-427-836-90500

  Query Match              1.5%;  Score 23.4;  DB 9;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 1.8e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1203 AGGGCACCATTCTCATCAACCGGGT 1227
           | ||||||||||||||||||||||||
Db       1 ACGGCACCATTCTCATCAACCGGGT 25


RESULT 23
US-60-427-836-238304
; Sequence 238304, Application US/60427836
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527
;  CURRENT APPLICATION NUMBER: US/60/427,836
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 238304
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-60-427-836-238304

  Query Match              1.5%;  Score 23.4;  DB 9;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 1.8e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1249 CATCGAGGAGCACAGCTGGGCGCAC 1273
           ||||||||||||||||||||||| |||
Db       1 CATCGAGGAGCACAGCTGGGCACAC 25


RESULT 24
US-60-427-836-454484
; Sequence 454484, Application US/60427836
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527
;  CURRENT APPLICATION NUMBER: US/60/427,836
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 454484
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-60-427-836-454484

  Query Match              1.5%;  Score 23.4;  DB 9;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 1.8e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1441 GGGCATCCACTGGTACTCGCAGCTG 1465
           ||||||||||||| ||||||||||||
Db       1 GGGCATCCACTGCTACTCGCAGCTG 25


RESULT 25
US-60-427-836-591791
; Sequence 591791, Application US/60427836
; GENERAL INFORMATION:
```

```
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527
;  CURRENT APPLICATION NUMBER: US/60/427,836
;  CURRENT FILING DATE:  2002-11-20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 591791
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-60-427-836-591791

  Query Match             1.5%;  Score 23.4;  DB 9;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 1.8e+05;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1235 TCGTGCTACGCGGTCATCGAGGAGC 1259
           ||||||||||| ||||||||||||
Db       1 TCGTGCTACGCAGTCATCGAGGAGC 25


Search completed: March 14, 2003, 01:10:16
Job time : 506 secs
```

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 13, 2003, 20:53:08 ; Search time 4362 Seconds
(without alignments)
10514.906 Million cell updates/sec

Title: US-10-001-844-3
Perfect score: 1576
Sequence: 1 gcgaggcagccagcgaggga.....gaggggcgcgggaggggcc 1576

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	50	3.2	50	6	AX146582	AX146582 Sequence
c	2	48.4	3.1	50	6	AX146613	AX146613 Sequence
c	3	48.4	3.1	50	6	AX146614	AX146614 Sequence
c	4	45.2	2.9	50	6	AX146616	AX146616 Sequence
	5	43.8	2.8	47	6	AX146608	AX146608 Sequence
	6	43.8	2.8	47	6	AX146609	AX146609 Sequence
	7	43.4	2.8	45	6	AX146612	AX146612 Sequence
c	8	42	2.7	50	6	AX146615	AX146615 Sequence
c	9	41.4	2.6	43	6	AX146617	AX146617 Sequence
	10	40.6	2.6	47	6	AX146611	AX146611 Sequence
	11	37.4	2.4	47	6	AX146610	AX146610 Sequence
	12	31.4	2.0	50	6	AX057285	AX057285 Sequence
c	13	27	1.7	27	9	HSA270316	AJ270316 Homo sapi
	14	26	1.6	50	6	AR178318	AR178318 Sequence
	15	26	1.6	50	6	AX323400	AX323400 Sequence
	16	25	1.6	33	6	I84406	I84406 Sequence 7
	17	24.6	1.6	50	6	AR199385	AR199385 Sequence
	18	24	1.5	24	6	AR063105	AR063105 Sequence
	19	24	1.5	24	6	AR122632	AR122632 Sequence
	20	24	1.5	24	6	AR164260	AR164260 Sequence
	21	24	1.5	24	6	AR208932	AR208932 Sequence
	22	24	1.5	45	6	I20760	I20760 Sequence 13
c	23	23.6	1.5	30	6	I84401	I84401 Sequence 2
c	24	23.6	1.5	31	6	A01419	A01419 Malaria par
c	25	22.4	1.4	32	6	A62993	A62993 Sequence 5
c	26	22.4	1.4	32	6	AR179068	AR179068 Sequence
	27	22.4	1.4	43	6	A28677	A28677 Oligonucleo
c	28	22.2	1.4	50	6	AX397845	AX397845 Sequence
	29	22	1.4	23	9	HSA270315	AJ270315 Homo sapi
c	30	22	1.4	29	6	AX146574	AX146574 Sequence
c	31	22	1.4	29	6	AX417112	AX417112 Sequence
c	32	22	1.4	44	6	A28674	A28674 dsRNA with
c	33	22	1.4	50	8	SSREP2	V01364 Scilla sibe
	34	21.8	1.4	35	6	I45648	I45648 Sequence 7
c	35	21.8	1.4	50	4	S72333	S72333 enkephalin
c	36	21.8	1.4	50	5	XELRGT2	M13246 X.laevis ri
	37	21.6	1.4	40	6	A98997	A98997 Sequence 5
	38	21.6	1.4	40	6	AR195314	AR195314 Sequence
c	39	21.6	1.4	48	6	A21991	A21991 oligonucleo
	40	21.6	1.4	49	6	A21992	A21992 oligonucleo
c	41	21.4	1.4	31	6	A62992	A62992 Sequence 4
c	42	21.4	1.4	31	6	AR179067	AR179067 Sequence
	43	21.4	1.4	50	6	AR137495	AR137495 Sequence
c	44	21.4	1.4	50	9	HSHLX1A1	X96914 H.sapiens H
	45	21.2	1.3	49	6	AX397846	AX397846 Sequence
c	46	21	1.3	47	6	A28685	A28685 Oligonucleo
c	47	21	1.3	50	6	AR032762	AR032762 Sequence
c	48	21	1.3	50	6	AR209426	AR209426 Sequence
c	49	21	1.3	50	6	AX199622	AX199622 Sequence
c	50	21	1.3	50	6	I29502	I29502 Sequence 37
c	51	21	1.3	50	6	I91176	I91176 Sequence 37
	52	20.8	1.3	43	6	AX002786	AX002786 Sequence
	53	20.8	1.3	43	6	AX149545	AX149545 Sequence
	54	20.8	1.3	46	6	A92687	A92687 Sequence 2
c	55	20.8	1.3	46	6	A92687	A92687 Sequence 2
c	56	20.8	1.3	47	6	AX002787	AX002787 Sequence
c	57	20.8	1.3	47	6	AX149555	AX149555 Sequence
	58	20.8	1.3	49	6	AX279826	AX279826 Sequence
c	59	20.8	1.3	50	6	A51123	A51123 Sequence 1
	60	20.8	1.3	50	6	AX199605	AX199605 Sequence
c	61	20.6	1.3	38	6	AX207477	AX207477 Sequence
	62	20.6	1.3	41	6	AX327055	AX327055 Sequence
c	63	20.6	1.3	43	6	A28678	A28678 Oligonucleo
c	64	20.6	1.3	45	6	A05111	A05111 Oligonucleo
	65	20.6	1.3	45	6	AR145517	AR145517 Sequence

	66	20.6	1.3	48	6	A47495
c	67	20.6	1.3	50	6	AX157874
c	68	20.4	1.3	30	6	A62990
	69	20.4	1.3	30	6	A62996
c	70	20.4	1.3	30	6	AR179065
	71	20.4	1.3	30	6	AR179071
c	72	20.4	1.3	30	6	AX104904
c	73	20.4	1.3	30	6	AX477343
c	74	20.4	1.3	35	6	AX104579
c	75	20.4	1.3	35	6	AX355144
c	76	20.4	1.3	40	6	AR184470
c	77	20.4	1.3	40	6	AX406837
	78	20.4	1.3	40	6	E13253
	79	20.4	1.3	41	6	AR106716
	80	20.4	1.3	41	6	AR202527
	81	20.4	1.3	44	6	AR199384
c	82	20.4	1.3	49	6	A21777
c	83	20.4	1.3	49	6	AX279808
	84	20.4	1.3	50	6	AR137494
c	85	20.2	1.3	40	6	AX472253
c	86	20.2	1.3	40	6	E05618
	87	20.2	1.3	46	6	A92686
c	88	20.2	1.3	46	6	A92686
	89	20.2	1.3	46	6	AR032473
	90	20.2	1.3	46	6	AR209137
	91	20.2	1.3	46	6	I29213
	92	20.2	1.3	46	6	I90887
c	93	20.2	1.3	47	6	AR071857
c	94	20.2	1.3	47	6	AR112597
	95	20.2	1.3	48	6	AR129985
	96	20.2	1.3	48	6	AR205077
	97	20.2	1.3	48	6	AX149574
	98	20	1.3	36	6	AX356948
c	99	20	1.3	42	6	AR116992
	100	20	1.3	45	6	AX080806
	101	20	1.3	45	6	AX191434
	102	20	1.3	45	6	AX403235
	103	20	1.3	45	6	I30008
	104	20	1.3	45	6	I93784
	105	20	1.3	47	12	SYNPRWA
c	106	20	1.3	50	6	AR024001
c	107	20	1.3	50	6	E12787
c	108	19.8	1.3	47	6	AX194734
	109	19.8	1.3	50	6	E00071
c	110	19.6	1.2	42	6	AR210880
c	111	19.6	1.2	45	6	AX027549
	112	19.6	1.2	46	6	E32206
c	113	19.6	1.2	48	6	AX207748
	114	19.6	1.2	50	6	I18452
	115	19.4	1.2	29	6	AX288078
c	116	19.4	1.2	33	6	A11717
	117	19.4	1.2	33	6	A11718
c	118	19.4	1.2	33	6	I14316
c	119	19.4	1.2	37	6	AX288079
	120	19.4	1.2	43	6	AR161404
	121	19.4	1.2	49	6	A04202
	122	19.4	1.2	49	6	AX157798
	123	19.4	1.2	50	6	AX202437
	124	19.2	1.2	24	6	AX327693
	125	19.2	1.2	33	6	AX236735
	126	19.2	1.2	36	6	AR193727
	127	19.2	1.2	41	6	E13926
	128	19.2	1.2	41	6	E16035
c	129	19.2	1.2	42	6	AR035287
	130	19.2	1.2	44	6	I31473
c	131	19.2	1.2	45	6	AX068135
c	132	19.2	1.2	45	6	I20761
c	133	19.2	1.2	47	6	AR030771
c	134	19.2	1.2	47	6	AR101775
c	135	19.2	1.2	48	6	AR073450
	136	19.2	1.2	48	6	AX222000
c	137	19.2	1.2	49	6	AR032793
c	138	19.2	1.2	49	6	AR209457

A47495 Sequence 2
AX157874 Sequence
A62990 Sequence 2
A62996 Sequence 8
AR179065 Sequence
AR179071 Sequence
AX104904 Sequence
AX477343 Sequence
AX104579 Sequence
AX355144 Sequence
AR184470 Sequence
AX406837 Sequence
E13253 Oligonucleo
AR106716 Sequence
AR202527 Sequence
AR199384 Sequence
A21777 oligonucleo
AX279808 Sequence
AR137494 Sequence
AX472253 Sequence
E05618 Primer for
A92686 Sequence 1
A92686 Sequence 1
AR032473 Sequence
AR209137 Sequence
I29213 Sequence 85
I90887 Sequence 85
AR071857 Sequence
AR112597 Sequence
AR129985 Sequence
AR205077 Sequence
AX149574 Sequence
AX356948 Sequence
AR116992 Sequence
AX080806 Sequence
AX191434 Sequence
AX403235 Sequence
I30008 Sequence 14
I93784 Sequence 14
M94403 Artificial
AR024001 Sequence
E12787 DNA probe f
AX194734 Sequence
E00071 Partial cDN
AR210880 Sequence
AX027549 Sequence
E32206 Method for
AX207748 Sequence
I18452 Sequence 75
AX288078 Sequence
A11717 oligonucleo
A11718 oligonucleo
I14316 Sequence 13
AX288079 Sequence
AR161404 Sequence
A04202 Nucleotide
AX157798 Sequence
AX202437 Sequence
AX327693 Sequence
AX236735 Sequence
AR193727 Sequence
E13926 Primer. 4/1
E16035 DNA primer
AR035287 Sequence
I31473 Sequence 38
AX068135 Sequence
I20761 Sequence 14
AR030771 Sequence
AR101775 Sequence
AR073450 Sequence
AX222000 Sequence
AR032793 Sequence
AR209457 Sequence

c	139	19.2	1.2	49	6	AX107693
c	140	19.2	1.2	49	6	I29533
c	141	19.2	1.2	49	6	I91207
c	142	19.2	1.2	50	6	AX160636
	143	19.2	1.2	50	6	I89841
	144	19	1.2	19	6	AR154250
	145	19	1.2	19	6	AR154254
	146	19	1.2	30	6	AX146573
	147	19	1.2	30	6	AX417111
	148	19	1.2	35	6	AX262313
c	149	19	1.2	36	6	A94124
c	150	19	1.2	36	6	AX014659
	151	19	1.2	36	6	AX402097
	152	19	1.2	36	6	AX403811
c	153	19	1.2	36	6	E50995
	154	19	1.2	38	6	A48819
	155	19	1.2	39	6	AR201228
	156	19	1.2	39	6	AX081636
	157	19	1.2	39	6	AX374817
c	158	19	1.2	41	6	AR206162
	159	19	1.2	43	6	AX180257
	160	19	1.2	44	6	E11299
	161	19	1.2	45	6	AX108066
	162	19	1.2	46	6	A38923
	163	19	1.2	46	6	AR054319
	164	19	1.2	46	9	HSU34722
	165	19	1.2	47	6	AX004825
	166	19	1.2	48	6	AX150279
c	167	19	1.2	50	6	AX057285
c	168	19	1.2	50	9	HSHLX1A4
c	169	18.8	1.2	32	6	AX067720
	170	18.8	1.2	38	6	AX108708
c	171	18.8	1.2	39	6	AR201228
c	172	18.8	1.2	39	6	AX080628
	173	18.8	1.2	40	6	AR055062
	174	18.8	1.2	40	6	AR156311
c	175	18.8	1.2	40	6	AX288072
	176	18.8	1.2	41	6	A38181
	177	18.8	1.2	42	6	AX288063
c	178	18.8	1.2	42	6	AX288064
	179	18.8	1.2	44	6	A21445
	180	18.8	1.2	44	6	A37850
	181	18.8	1.2	44	6	AR069888
	182	18.8	1.2	44	6	AR099285
	183	18.8	1.2	44	6	AR124169
	184	18.8	1.2	44	6	E43912
c	185	18.8	1.2	45	6	AX068136
c	186	18.8	1.2	45	6	AX068137
c	187	18.8	1.2	45	6	AX068139
	188	18.8	1.2	45	6	E02957
	189	18.8	1.2	46	6	AX190432
c	190	18.8	1.2	47	6	AR055043
c	191	18.8	1.2	47	6	AR156292
	192	18.8	1.2	48	6	AR019022
	193	18.8	1.2	48	6	AR130422
	194	18.8	1.2	48	6	AX278749
	195	18.8	1.2	48	6	AX279916
	196	18.8	1.2	49	6	AX279656
	197	18.8	1.2	49	6	AX279677
	198	18.8	1.2	49	6	AX279825
	199	18.8	1.2	50	6	AX351171
	200	18.6	1.2	25	6	AR028113
	201	18.6	1.2	25	6	AR030289
	202	18.6	1.2	25	6	I42108
	203	18.6	1.2	28	6	AX010555
	204	18.6	1.2	36	6	AX050277
	205	18.6	1.2	38	6	AX059027
	206	18.6	1.2	44	6	A94787
	207	18.6	1.2	44	6	E11304
	208	18.6	1.2	45	6	AR118818
c	209	18.6	1.2	45	6	AX080806
c	210	18.6	1.2	45	6	AX191434
c	211	18.6	1.2	45	6	AX403235

AX107693 Sequence
I29533 Sequence 40
I91207 Sequence 40
AX160636 Sequence
I89841 Sequence 12
AR154250 Sequence
AR154254 Sequence
AX146573 Sequence
AX417111 Sequence
AX262313 Sequence
A94124 Sequence 2
AX014659 Sequence
AX402097 Sequence
AX403811 Sequence
E50995 Hedgehog pr
A48819 Sequence 11
AR201228 Sequence
AX081636 Sequence
AX374817 Sequence
AR206162 Sequence
AX180257 Sequence
E11299 PCR primer
AX108066 Sequence
A38923 Sequence 10
AR054319 Sequence
U34722 Homo sapien
AX004825 Sequence
AX150279 Sequence
AX057285 Sequence
X96921 H.sapiens H
AX067720 Sequence
AX108708 Sequence
AR201228 Sequence
AX080628 Sequence
AR055062 Sequence
AR156311 Sequence
AX288072 Sequence
A38181 Sequence 25
AX288063 Sequence
AX288064 Sequence
A21445 oligonucleo
A37850 Sequence 20
AR069888 Sequence
AR099285 Sequence
AR124169 Sequence
E43912 Novel vecto
AX068136 Sequence
AX068137 Sequence
AX068139 Sequence
E02957 Signal repe
AX190432 Sequence
AR055043 Sequence
AR156292 Sequence
AR019022 Sequence
AR130422 Sequence
AX278749 Sequence
AX279916 Sequence
AX279656 Sequence
AX279677 Sequence
AX279825 Sequence
AX351171 Sequence
AR028113 Sequence
AR030289 Sequence
I42108 Sequence 3
AX010555 Sequence
AX050277 Sequence
AX059027 Sequence
A94787 Sequence 31
E11304 PCR primer
AR118818 Sequence
AX080806 Sequence
AX191434 Sequence
AX403235 Sequence

	212	18.6	1.2	48	6 A47501
	213	18.6	1.2	48	6 AX207747
c	214	18.6	1.2	49	6 AR014134
c	215	18.6	1.2	49	6 AX278779
	216	18.6	1.2	49	6 AX279676
c	217	18.6	1.2	49	6 AX279946
c	218	18.6	1.2	49	6 I18451
c	219	18.6	1.2	50	6 AR032851
c	220	18.6	1.2	50	6 AR209515
c	221	18.6	1.2	50	6 AX157405
c	222	18.6	1.2	50	6 I29591
c	223	18.6	1.2	50	6 I91265
c	224	18.4	1.2	28	6 AX104578
c	225	18.4	1.2	28	6 AX355143
	226	18.4	1.2	31	6 AX249029
	227	18.4	1.2	32	6 AX288071
	228	18.4	1.2	33	6 AX068142
	229	18.4	1.2	36	6 AX356940
c	230	18.4	1.2	42	6 I00662
c	231	18.4	1.2	43	6 A50977
	232	18.4	1.2	44	6 AR086388
c	233	18.4	1.2	44	6 AX001092
	234	18.4	1.2	45	6 AX231579
	235	18.4	1.2	45	6 I60574
c	236	18.4	1.2	47	6 AX211584
	237	18.4	1.2	47	6 AX429816
c	238	18.4	1.2	47	6 I84675
c	239	18.4	1.2	48	6 AX207754
	240	18.4	1.2	48	6 AX253583
	241	18.4	1.2	49	6 AR032793
	242	18.4	1.2	49	6 AR209457
	243	18.4	1.2	49	6 AX279597
c	244	18.4	1.2	49	6 AX279820
	245	18.4	1.2	49	6 I29533
	246	18.4	1.2	49	6 I91207
c	247	18.4	1.2	50	6 A07724
c	248	18.4	1.2	50	6 A10023
c	249	18.4	1.2	50	6 AR032514
	250	18.4	1.2	50	6 AR032869
c	251	18.4	1.2	50	6 AR209178
	252	18.4	1.2	50	6 AR209533
	253	18.4	1.2	50	6 AX019535
	254	18.4	1.2	50	6 AX162468
c	255	18.4	1.2	50	6 AX165817
c	256	18.4	1.2	50	6 AX426994
c	257	18.4	1.2	50	6 I29254
	258	18.4	1.2	50	6 I29609
c	259	18.4	1.2	50	6 I90928
	260	18.4	1.2	50	6 I91283
	261	18.2	1.2	24	6 AR063245
c	262	18.2	1.2	25	6 E16681
	263	18.2	1.2	35	6 AR202292
	264	18.2	1.2	39	6 AR033894
	265	18.2	1.2	39	6 AR175027
	266	18.2	1.2	39	6 AX032459
	267	18.2	1.2	39	6 E11415
c	268	18.2	1.2	40	6 AR079790
c	269	18.2	1.2	40	6 AR081320
c	270	18.2	1.2	40	6 AR170680
	271	18.2	1.2	41	6 A38185
	272	18.2	1.2	42	6 AX077421
c	273	18.2	1.2	43	6 AX456423
c	274	18.2	1.2	45	6 AR071841
c	275	18.2	1.2	45	6 AR112581
	276	18.2	1.2	45	9 HSBIA1G1B
	277	18.2	1.2	46	6 AR032572
	278	18.2	1.2	46	6 AR209236
	279	18.2	1.2	46	6 I29312
	280	18.2	1.2	46	6 I90986
	281	18.2	1.2	47	6 AX278807
	282	18.2	1.2	47	6 AX279974
	283	18.2	1.2	47	10 MUSIGHYV
c	284	18.2	1.2	48	6 A62955

A47501 Sequence 8
AX207747 Sequence
AR014134 Sequence
AX278779 Sequence
AX279676 Sequence
AX279946 Sequence
I18451 Sequence 74
AR032851 Sequence
AR209515 Sequence
AX157405 Sequence
I29591 Sequence 46
I91265 Sequence 46
AX104578 Sequence
AX355143 Sequence
AX249029 Sequence
AX288071 Sequence
AX068142 Sequence
AX356940 Sequence
I00662 Sequence 3
A50977 Sequence 18
AR086388 Sequence
AX001092 Sequence
AX231579 Sequence
I60574 Sequence 31
AX211584 Sequence
AX429816 Sequence
I84675 Sequence 9
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AX253583 Sequence
AR032793 Sequence
AR209457 Sequence
AX279597 Sequence
AX279820 Sequence
I29533 Sequence 40
I91207 Sequence 40
A07724 Oligonucleo
A10023 Nucleotide
AR032514 Sequence
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AR209178 Sequence
AR209533 Sequence
AX019535 Sequence
AX162468 Sequence
AX165817 Sequence
AX426994 Sequence
I29254 Sequence 12
I29609 Sequence 48
I90928 Sequence 12
I91283 Sequence 48
AR063245 Sequence
E16681 Primer. 7/1
AR202292 Sequence
AR033894 Sequence
AR175027 Sequence
AX032459 Sequence
E11415 Primer. 9/1
AR079790 Sequence
AR081320 Sequence
AR170680 Sequence
A38185 Sequence 29
AX077421 Sequence
AX456423 Sequence
AR071841 Sequence
AR112581 Sequence
X72166 H.sapiens (
AR032572 Sequence
AR209236 Sequence
I29312 Sequence 18
I90986 Sequence 18
AX278807 Sequence
AX279974 Sequence
M22392 Mouse Ig ge
A62955 Sequence 19

	285	18.2	1.2	48	6 AR202324
	286	18.2	1.2	48	6 AX059009
	287	18.2	1.2	48	6 AX229277
	288	18.2	1.2	48	6 AX453570
	289	18.2	1.2	48	6 I06257
c	290	18.2	1.2	48	9 S34436
c	291	18.2	1.2	49	6 AX279658
	292	18.2	1.2	49	6 AX279675
	293	18.2	1.2	49	6 AX279727
	294	18.2	1.2	50	6 AR032719
c	295	18.2	1.2	50	6 AR145250
	296	18.2	1.2	50	6 AR209383
c	297	18.2	1.2	50	6 AX161854
c	298	18.2	1.2	50	6 AX204297
	299	18.2	1.2	50	6 I29459
	300	18.2	1.2	50	6 I91133
	301	18.2	1.2	50	10 MMVIMV47
c	302	18	1.1	18	6 AR154251
	303	18	1.1	27	6 AR040322
	304	18	1.1	36	6 AR084542
c	305	18	1.1	36	6 AR206158
c	306	18	1.1	39	6 AR200691
	307	18	1.1	39	6 I06515
	308	18	1.1	41	6 A38183
	309	18	1.1	42	6 A42175
	310	18	1.1	42	6 A50686
	311	18	1.1	42	6 A50722
	312	18	1.1	42	6 AR004820
	313	18	1.1	42	6 AR035286
	314	18	1.1	42	6 AR051254
	315	18	1.1	42	6 AR083317
	316	18	1.1	42	6 AR116201
c	317	18	1.1	42	6 AX009738
	318	18	1.1	42	6 I28383
	319	18	1.1	42	6 I71226
c	320	18	1.1	43	6 A04391
	321	18	1.1	43	6 A81880
	322	18	1.1	43	6 AR120683
	323	18	1.1	43	6 AX322481
	324	18	1.1	43	6 I34859
	325	18	1.1	44	6 AX297758
	326	18	1.1	45	6 AX068135
	327	18	1.1	46	6 AR157388
	328	18	1.1	46	6 AX004805
	329	18	1.1	47	6 AX004827
c	330	18	1.1	47	6 AX195051
	331	18	1.1	48	6 AR032591
	332	18	1.1	48	6 AR184250
	333	18	1.1	48	6 AR184371
	334	18	1.1	48	6 AR209255
	335	18	1.1	48	6 AX127962
c	336	18	1.1	48	6 AX253582
c	337	18	1.1	48	6 E13605
	338	18	1.1	48	6 I29331
	339	18	1.1	48	6 I91005
	340	18	1.1	49	6 AX279622
	341	18	1.1	49	6 AX279645
	342	18	1.1	50	4 F292317S04
	343	18	1.1	50	6 AR014135
	344	18	1.1	50	6 AR032762
c	345	18	1.1	50	6 AR032862
	346	18	1.1	50	6 AR162078
	347	18	1.1	50	6 AR166603
	348	18	1.1	50	6 AR209426
c	349	18	1.1	50	6 AR209526
c	350	18	1.1	50	6 AX019536
c	351	18	1.1	50	6 AX159942
c	352	18	1.1	50	6 AX160484
	353	18	1.1	50	6 BD002070
	354	18	1.1	50	6 I29502
c	355	18	1.1	50	6 I29602
	356	18	1.1	50	6 I31257
	357	18	1.1	50	6 I91176

AR202324 Sequence
AX059009 Sequence
AX229277 Sequence
AX453570 Sequence
I06257 Sequence 15
S34436 glycoprotei
AX279658 Sequence
AX279675 Sequence
AX279727 Sequence
AR032719 Sequence
AR145250 Sequence
AR209383 Sequence
AX161854 Sequence
AX204297 Sequence
I29459 Sequence 33
I91133 Sequence 33
X89164 M.musculus
AR154251 Sequence
AR040322 Sequence
AR084542 Sequence
AR206158 Sequence
AR200691 Sequence
I06515 Sequence 19
A38183 Sequence 27
A42175 Sequence 65
A50686 Sequence 25
A50722 Sequence 16
AR004820 Sequence
AR035286 Sequence
AR051254 Sequence
AR083317 Sequence
AR116201 Sequence
AX009738 Sequence
I28383 Sequence 22
I71226 Sequence 23
A04391 Oligonucleo
A81880 Sequence 11
AR120683 Sequence
AX322481 Sequence
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AX297758 Sequence
AX068135 Sequence
AR157388 Sequence
AX004805 Sequence
AX004827 Sequence
AX195051 Sequence
AR032591 Sequence
AR184250 Sequence
AR184371 Sequence
AR209255 Sequence
AX127962 Sequence
AX253582 Sequence
E13605 Linker. 4/1
I29331 Sequence 20
I91005 Sequence 20
AX279622 Sequence
AX279645 Sequence
AF292320 Bos tauru
AR014135 Sequence
AR032762 Sequence
AR032862 Sequence
AR162078 Sequence
AR166603 Sequence
AR209426 Sequence
AR209526 Sequence
AX019536 Sequence
AX159942 Sequence
AX160484 Sequence
BD002070 Method of
I29502 Sequence 37
I29602 Sequence 47
I31257 Sequence 16
I91176 Sequence 37

c 358	18	1.1	50	6	I91276
c 359	17.8	1.1	21	6	AR177692
360	17.8	1.1	31	6	AX248046
361	17.8	1.1	31	6	AX249447
c 362	17.8	1.1	39	6	AX202296
363	17.8	1.1	39	6	AX250377
364	17.8	1.1	44	6	E11301
c 365	17.8	1.1	45	6	AR032679
c 366	17.8	1.1	45	6	AR040714
367	17.8	1.1	45	6	AR141182
368	17.8	1.1	45	6	AR141183
c 369	17.8	1.1	45	6	AR209343
c 370	17.8	1.1	45	6	I29419
c 371	17.8	1.1	45	6	I91093
372	17.8	1.1	46	6	A98794
c 373	17.8	1.1	46	6	I12506
374	17.8	1.1	46	6	I12507
c 375	17.8	1.1	46	6	I12508
376	17.8	1.1	46	6	I12509
377	17.8	1.1	47	6	AR086675
378	17.8	1.1	47	6	AX252287
c 379	17.8	1.1	47	10	MUSIGHYV
380	17.8	1.1	48	6	A18448
381	17.8	1.1	48	6	AR000192
382	17.8	1.1	48	6	AX207753
383	17.8	1.1	49	6	A27752
384	17.8	1.1	50	6	A14174
385	17.8	1.1	50	6	A14176
386	17.8	1.1	50	6	A14178
387	17.8	1.1	50	6	A14198
c 388	17.8	1.1	50	6	AR032925
c 389	17.8	1.1	50	6	AR209589
390	17.8	1.1	50	6	AX157456
c 391	17.8	1.1	50	6	I29665
c 392	17.8	1.1	50	6	I91339
393	17.8	1.1	50	9	AF057500
394	17.8	1.1	50	9	AF057514
395	17.8	1.1	50	9	AF176985S5
396	17.8	1.1	50	9	HSHLX1D4
397	17.6	1.1	28	6	AX010556
398	17.6	1.1	28	6	AX183895
399	17.6	1.1	30	6	AX343761
c 400	17.6	1.1	31	6	AX003697
c 401	17.6	1.1	31	6	BD002916
c 402	17.6	1.1	32	6	AR182071
c 403	17.6	1.1	34	6	A00833
c 404	17.6	1.1	34	6	A16002
405	17.6	1.1	34	6	AR003387
406	17.6	1.1	34	6	I21176
407	17.6	1.1	34	6	I74443
c 408	17.6	1.1	36	6	A47503
c 409	17.6	1.1	36	6	AR123709
410	17.6	1.1	36	6	AR206158
c 411	17.6	1.1	36	6	I34917
412	17.6	1.1	40	6	A69174
c 413	17.6	1.1	41	6	A65145
414	17.6	1.1	41	6	AR032631
415	17.6	1.1	41	6	AR209295
c 416	17.6	1.1	41	6	AX015113
c 417	17.6	1.1	41	6	AX174849
418	17.6	1.1	41	6	E02634
419	17.6	1.1	41	6	I29371
420	17.6	1.1	41	6	I91045
421	17.6	1.1	42	6	AX068138
422	17.6	1.1	42	10	MUSMHAB05
c 423	17.6	1.1	44	6	A69175
424	17.6	1.1	44	6	AR032451
425	17.6	1.1	44	6	AR079003
426	17.6	1.1	44	6	AR209115
c 427	17.6	1.1	44	6	I04406
c 428	17.6	1.1	44	6	I04435
429	17.6	1.1	44	6	I29191
430	17.6	1.1	44	6	I90865

I91276 Sequence 47
AR177692 Sequence
AX248046 Sequence
AX249447 Sequence
AX202296 Sequence
AX250377 Sequence
E11301 PCR primer
AR032679 Sequence
AR040714 Sequence
AR141182 Sequence
AR141183 Sequence
AR209343 Sequence
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I91093 Sequence 29
A98794 Sequence 27
I12506 Sequence 28
I12507 Sequence 29
I12508 Sequence 31
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AR086675 Sequence
AX252287 Sequence
M22392 Mouse Ig ge
A18448 oligonucleo
AR000192 Sequence
AX207753 Sequence
A27752 Plasmid seq
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A14176 vectorette
A14178 vectorette
A14198 specific ve
AR032925 Sequence
AR209589 Sequence
AX157456 Sequence
I29665 Sequence 53
I91339 Sequence 53
AF057500 Homo sapi
AF057514 Homo sapi
AF176989 Homo sapi
X96920 H.sapiens H
AX010556 Sequence
AX183895 Sequence
AX343761 Sequence
AX003697 Sequence
BD002916 Gene comp
AR182071 Sequence
A00833 Adapter (re
A16002 adapter mol
AR003387 Sequence
I21176 Sequence 22
I74443 Sequence 22
A47503 Sequence 10
AR123709 Sequence
AR206158 Sequence
I34917 Sequence 3
A69174 Sequence 92
A65145 Sequence 1
AR032631 Sequence
AR209295 Sequence
AX015113 Sequence
AX174849 Sequence
E02634 linker. 9/1
I29371 Sequence 24
I91045 Sequence 24
AX068138 Sequence
M86506 M.musculus
A69175 Sequence 93
AR032451 Sequence
AR079003 Sequence
AR209115 Sequence
I04406 Sequence 4
I04435 Sequence 33
I29191 Sequence 63
I90865 Sequence 63

c 431	17.6	1.1	45	6	AR026070
432	17.6	1.1	45	6	AR085812
433	17.6	1.1	45	6	AX010369
c 434	17.6	1.1	45	6	AX010370
435	17.6	1.1	45	6	AX472849
c 436	17.6	1.1	45	6	AX472850
c 437	17.6	1.1	45	6	I92648
c 438	17.6	1.1	46	1	AFU430234
439	17.6	1.1	46	6	A38210
c 440	17.6	1.1	46	6	AX157711
441	17.6	1.1	46	6	I22397
c 442	17.6	1.1	47	6	A89623
c 443	17.6	1.1	47	6	A93558
c 444	17.6	1.1	47	6	AR176118
c 445	17.6	1.1	47	6	AR182398
c 446	17.6	1.1	47	6	AX194728
c 447	17.6	1.1	48	6	A14922
448	17.6	1.1	48	6	A19431
449	17.6	1.1	48	6	AR026089
450	17.6	1.1	48	6	AR195131
451	17.6	1.1	48	6	I13412
c 452	17.6	1.1	48	9	S68399
453	17.6	1.1	49	6	AR032650
454	17.6	1.1	49	6	AR209314
455	17.6	1.1	49	6	AX278769
456	17.6	1.1	49	6	AX279936
457	17.6	1.1	49	6	I29390
458	17.6	1.1	49	6	I91064
459	17.6	1.1	49	9	HUMNTCOF25
c 460	17.6	1.1	49	10	MUSIGHSWIU
c 461	17.6	1.1	50	6	A69173
462	17.6	1.1	50	6	AR032912
c 463	17.6	1.1	50	6	AR032979
464	17.6	1.1	50	6	AR091514
465	17.6	1.1	50	6	AR154394
466	17.6	1.1	50	6	AR157999
467	17.6	1.1	50	6	AR174322
468	17.6	1.1	50	6	AR183306
469	17.6	1.1	50	6	AR209576
c 470	17.6	1.1	50	6	AR209643
471	17.6	1.1	50	6	AR210478
472	17.6	1.1	50	6	AX080358
473	17.6	1.1	50	6	AX159414
c 474	17.6	1.1	50	6	AX199605
c 475	17.6	1.1	50	6	AX233378
476	17.6	1.1	50	6	I29652
c 477	17.6	1.1	50	6	I29719
478	17.6	1.1	50	6	I91326
c 479	17.6	1.1	50	6	I91393
480	17.6	1.1	50	10	MMU41953
481	17.4	1.1	26	6	A94123
482	17.4	1.1	26	6	AX014658
483	17.4	1.1	26	6	E50994
c 484	17.4	1.1	27	6	E04986
485	17.4	1.1	27	6	E04987
486	17.4	1.1	28	6	AR199381
487	17.4	1.1	30	6	E14027
c 488	17.4	1.1	31	6	AX248134
c 489	17.4	1.1	31	6	AX248140
490	17.4	1.1	31	6	AX248597
491	17.4	1.1	31	6	AX248880
492	17.4	1.1	31	6	AX249132
493	17.4	1.1	35	6	AR049526
494	17.4	1.1	35	6	AR065731
495	17.4	1.1	35	6	AR171308
496	17.4	1.1	35	6	AX080146
497	17.4	1.1	35	6	AX201766
c 498	17.4	1.1	36	6	AR104430
499	17.4	1.1	36	6	I78169
c 500	17.4	1.1	37	6	AX298019
501	17.4	1.1	38	6	AR021293
502	17.4	1.1	38	6	AR129336
503	17.4	1.1	38	6	AR160091

AR026070 Sequence
AR085812 Sequence
AX010369 Sequence
AX010370 Sequence
AX472849 Sequence
AX472850 Sequence
I92648 Sequence 22
AJ430234 Archaeogl
A38210 Sequence 54
AX157711 Sequence
I22397 Sequence 5
A89623 Sequence 7
A93558 Sequence 3
AR176118 Sequence
AR182398 Sequence
AX194728 Sequence
A14922 oligonucleo
A19431 AB1024 olig
AR026089 Sequence
AR195131 Sequence
I13412 Sequence 14
S68399 TCR V beta
AR032650 Sequence
AR209314 Sequence
AX278769 Sequence
AX279936 Sequence
I29390 Sequence 26
I91064 Sequence 26
U84664 Human putat
M26303 Mus musculu
A69173 Sequence 91
AR032912 Sequence
AR032979 Sequence
AR091514 Sequence
AR154394 Sequence
AR157999 Sequence
AR174322 Sequence
AR183306 Sequence
AR209576 Sequence
AR209643 Sequence
AR210478 Sequence
AX080358 Sequence
AX159414 Sequence
AX199605 Sequence
AX233378 Sequence
I29652 Sequence 52
I29719 Sequence 59
I91326 Sequence 52
I91393 Sequence 59
U41953 Mus musculu
A94123 Sequence 1
AX014658 Sequence
E50994 Hedgehog pr
E04986 DNA sequenc
E04987 DNA sequenc
AR199381 Sequence
E14027 Probe. 7/19
AX248134 Sequence
AX248140 Sequence
AX248597 Sequence
AX248880 Sequence
AX249132 Sequence
AR049526 Sequence
AR065731 Sequence
AR171308 Sequence
AX080146 Sequence
AX201766 Sequence
AR104430 Sequence
I78169 Sequence 87
AX298019 Sequence
AR021293 Sequence
AR129336 Sequence
AR160091 Sequence

c 504	17.4	1.1	39	6	AX350023
505	17.4	1.1	41	6	A13533
c 506	17.4	1.1	41	6	A13534
507	17.4	1.1	41	6	AX006150
508	17.4	1.1	41	6	AX327045
c 509	17.4	1.1	41	6	AX327070
510	17.4	1.1	42	6	AX166901
511	17.4	1.1	42	6	E26049
c 512	17.4	1.1	42	6	I95011
c 513	17.4	1.1	43	6	AX483436
514	17.4	1.1	43	6	I00832
515	17.4	1.1	43	6	I00841
516	17.4	1.1	43	6	I06027
517	17.4	1.1	44	6	AR032540
518	17.4	1.1	44	6	AR209204
c 519	17.4	1.1	44	6	AX112010
520	17.4	1.1	44	6	I29280
521	17.4	1.1	44	6	I90954
c 522	17.4	1.1	44	9	HUMTCVD1BL
523	17.4	1.1	44	9	HUMTCCVJ29
524	17.4	1.1	45	6	A05111
c 525	17.4	1.1	45	6	AR032587
c 526	17.4	1.1	45	6	AR168032
c 527	17.4	1.1	45	6	AR204803
c 528	17.4	1.1	45	6	AR209251
c 529	17.4	1.1	45	6	I29327
c 530	17.4	1.1	45	6	I91001
531	17.4	1.1	46	6	I27049
532	17.4	1.1	47	6	AR032401
533	17.4	1.1	47	6	AR209065
534	17.4	1.1	47	6	AX004828
535	17.4	1.1	47	6	AX004830
536	17.4	1.1	47	6	AX080981
537	17.4	1.1	47	6	AX404877
538	17.4	1.1	47	6	I29141
539	17.4	1.1	47	6	I90815
c 540	17.4	1.1	48	6	A47501
541	17.4	1.1	48	6	A62956
542	17.4	1.1	48	6	A97298
543	17.4	1.1	48	6	AX150273
544	17.4	1.1	49	6	I95010
545	17.4	1.1	50	6	A60808
546	17.4	1.1	50	6	AX156889
547	17.4	1.1	50	6	AX160148
548	17.4	1.1	50	6	AX160470
549	17.4	1.1	50	6	AX160472
c 550	17.4	1.1	50	6	AX161340
551	17.4	1.1	50	6	AX161968
c 552	17.4	1.1	50	6	AX190233
c 553	17.4	1.1	50	6	AX199626
c 554	17.4	1.1	50	6	AX202435
555	17.4	1.1	50	6	AX453556
556	17.4	1.1	50	6	I23716
557	17.4	1.1	50	6	I24075
558	17.4	1.1	50	6	I27200
559	17.4	1.1	50	10	MMU41938
c 560	17.2	1.1	24	6	AR028416
c 561	17.2	1.1	24	6	AR130926
c 562	17.2	1.1	24	6	AR161892
563	17.2	1.1	30	6	AX104905
c 564	17.2	1.1	30	6	AX104905
565	17.2	1.1	30	6	E04679
c 566	17.2	1.1	30	6	E04682
567	17.2	1.1	30	6	E30036
c 568	17.2	1.1	32	6	AX009737
569	17.2	1.1	33	6	AX011221
c 570	17.2	1.1	34	6	A14039
571	17.2	1.1	34	6	A14040
c 572	17.2	1.1	34	6	A31929
c 573	17.2	1.1	35	6	AR159970
c 574	17.2	1.1	35	6	AX028956
575	17.2	1.1	35	6	E30638
576	17.2	1.1	35	6	E31247

AX350023 Sequence
A13533 oligonucleo
A13534 oligonucleo
AX006150 Sequence
AX327045 Sequence
AX327070 Sequence
AX166901 Sequence
E26049 Peptide fra
I95011 Sequence 28
AX483436 Sequence
I00832 Sequence 3
I00841 Sequence 4
I06027 Sequence 1
AR032540 Sequence
AR209204 Sequence
AX112010 Sequence
I29280 Sequence 15
I90954 Sequence 15
L32409 Human (clon
L39496 Homo sapien
A05111 Oligonucleo
AR032587 Sequence
AR168032 Sequence
AR204803 Sequence
AR209251 Sequence
I29327 Sequence 19
I91001 Sequence 19
I27049 Sequence 70
AR032401 Sequence
AR209065 Sequence
AX004828 Sequence
AX004830 Sequence
AX080981 Sequence
AX404877 Sequence
I29141 Sequence 13
I90815 Sequence 13
A47501 Sequence 8
A62956 Sequence 19
A97298 Sequence 15
AX150273 Sequence
I95010 Sequence 27
A60808 Sequence 11
AX156889 Sequence
AX160148 Sequence
AX160470 Sequence
AX160472 Sequence
AX161340 Sequence
AX161968 Sequence
AX190233 Sequence
AX199626 Sequence
AX202435 Sequence
AX453556 Sequence
I23716 Sequence 11
I24075 Sequence 11
I27200 Sequence 11
U41938 Mus musculu
AR028416 Sequence
AR130926 Sequence
AR161892 Sequence
AX104905 Sequence
AX104905 Sequence
E04679 Synthetic n
E04682 Synthetic n
E30036 Human BMP-4
AX009737 Sequence
AX011221 Sequence
A14039 Nucleotide
A14040 Nucleotide
A31929 Synthetic p
AR159970 Sequence
AX028956 Sequence
E30638 Antibody an
E31247 Device for

577	17.2	1.1	36	6	A83219
578	17.2	1.1	36	6	AR182945
579	17.2	1.1	37	6	AR108958
c 580	17.2	1.1	39	6	AX283647
581	17.2	1.1	39	10	S86273
c 582	17.2	1.1	40	6	A19014
583	17.2	1.1	40	6	I12505
584	17.2	1.1	41	6	A38184
585	17.2	1.1	41	6	A38186
586	17.2	1.1	41	6	A38204
587	17.2	1.1	41	6	AR016437
c 588	17.2	1.1	42	6	AR058948
589	17.2	1.1	42	6	AR097752
c 590	17.2	1.1	42	6	AR105222
c 591	17.2	1.1	42	6	AR119143
c 592	17.2	1.1	42	6	AR123514
c 593	17.2	1.1	42	6	AR138167
c 594	17.2	1.1	42	6	AR176728
c 595	17.2	1.1	42	6	AR198299
c 596	17.2	1.1	42	6	AX193989
c 597	17.2	1.1	42	6	AX469992
c 598	17.2	1.1	43	6	AR013755
c 599	17.2	1.1	43	6	AX135623
600	17.2	1.1	43	6	AX466471
601	17.2	1.1	44	6	E11302
602	17.2	1.1	44	6	E23267
c 603	17.2	1.1	44	6	I82392
c 604	17.2	1.1	45	6	AR145517
c 605	17.2	1.1	45	6	AX027553
c 606	17.2	1.1	46	6	A98793
607	17.2	1.1	46	6	AR032571
608	17.2	1.1	46	6	AR209235
609	17.2	1.1	46	6	I29311
610	17.2	1.1	46	6	I90985
c 611	17.2	1.1	47	6	AR169657
612	17.2	1.1	47	6	AX004829
613	17.2	1.1	47	6	AX010672
614	17.2	1.1	47	6	AX128389
615	17.2	1.1	47	6	AX254660
616	17.2	1.1	47	6	E58964
617	17.2	1.1	48	6	A16034
618	17.2	1.1	48	6	AR117273
619	17.2	1.1	48	6	AR135812
c 620	17.2	1.1	48	6	AR135812
621	17.2	1.1	48	6	AR135814
c 622	17.2	1.1	48	6	AR135814
623	17.2	1.1	48	6	AR135816
c 624	17.2	1.1	48	6	AR135816
625	17.2	1.1	48	9	HUMTCRVJ34
c 626	17.2	1.1	48	9	HUMTCRVJ34
627	17.2	1.1	48	9	S81467
c 628	17.2	1.1	49	6	AX021173
c 629	17.2	1.1	49	6	AX060432
630	17.2	1.1	49	6	AX278759
631	17.2	1.1	49	6	AX279926
632	17.2	1.1	49	6	I20745
633	17.2	1.1	50	6	A45017
c 634	17.2	1.1	50	6	AR032500
c 635	17.2	1.1	50	6	AR032719
c 636	17.2	1.1	50	6	AR209164
c 637	17.2	1.1	50	6	AR209383
638	17.2	1.1	50	6	AX160730
639	17.2	1.1	50	6	AX165889
c 640	17.2	1.1	50	6	AX199624
c 641	17.2	1.1	50	6	AX202437
642	17.2	1.1	50	6	AX351170
643	17.2	1.1	50	6	AX351174
c 644	17.2	1.1	50	6	I29240
c 645	17.2	1.1	50	6	I29459
c 646	17.2	1.1	50	6	I90914
c 647	17.2	1.1	50	6	I91133
c 648	17.2	1.1	50	9	F220249S01
649	17.2	1.1	50	9	HSAJ4654

A83219 Sequence 39
AR182945 Sequence
AR108958 Sequence
AX283647 Sequence
S86273 TCR V beta
A19014 Oligonucleo
I12505 Sequence 26
A38184 Sequence 28
A38186 Sequence 30
A38204 Sequence 48
AR016437 Sequence
AR058948 Sequence
AR097752 Sequence
AR105222 Sequence
AR119143 Sequence
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AR138167 Sequence
AR176728 Sequence
AR198299 Sequence
AX193989 Sequence
AX469992 Sequence
AR013755 Sequence
AX135623 Sequence
AX466471 Sequence
E11302 PCR primer
E23267 Anti-HBs mo
I82392 Sequence 28
AR145517 Sequence
AX027553 Sequence
A98793 Sequence 26
AR032571 Sequence
AR209235 Sequence
I29311 Sequence 18
I90985 Sequence 18
AR169657 Sequence
AX004829 Sequence
AX010672 Sequence
AX128389 Sequence
AX254660 Sequence
E58964 Novel pepti
A16034 oligonucleo
AR117273 Sequence
AR135812 Sequence
AR135812 Sequence
AR135814 Sequence
AR135814 Sequence
AR135816 Sequence
AR135816 Sequence
L39572 Homo sapien
L39572 Homo sapien
S81467 T cell anti
AX021173 Sequence
AX060432 Sequence
AX278759 Sequence
AX279926 Sequence
I20745 Sequence 10
A45017 Sequence 4
AR032500 Sequence
AR032719 Sequence
AR209164 Sequence
AR209383 Sequence
AX160730 Sequence
AX165889 Sequence
AX199624 Sequence
AX202437 Sequence
AX351170 Sequence
AX351174 Sequence
I29240 Sequence 11
I29459 Sequence 33
I90914 Sequence 11
I91133 Sequence 33
AF220249 Homo sapi
AJ224654 Homo sapi

c 650	17.2	1.1	50	9	HSTFE3IA4	X84968 H.sapiens t
c 651	17.2	1.1	50	9	HUMTCCVJ70	L39537 Homo sapien
652	17.2	1.1	50	9	S72295S4	S72292 GPIa=platel
653	17	1.1	25	6	AR201287	AR201287 Sequence
654	17	1.1	26	6	E16680	E16680 Primer. 7/1
c 655	17	1.1	29	6	I55135	I55135 Sequence 12
656	17	1.1	30	6	AX328457	AX328457 Sequence
c 657	17	1.1	32	6	A32995	A32995 Synthetic P
c 658	17	1.1	32	6	A32998	A32998 Synthetic P
659	17	1.1	32	6	AX281125	AX281125 Sequence
c 660	17	1.1	32	6	AX357174	AX357174 Sequence
c 661	17	1.1	33	6	A14926	A14926 oligonucleo
662	17	1.1	33	6	AR093707	AR093707 Sequence
c 663	17	1.1	33	6	AR106717	AR106717 Sequence
664	17	1.1	33	6	AR139631	AR139631 Sequence
665	17	1.1	33	6	AR154143	AR154143 Sequence
c 666	17	1.1	33	6	AR202528	AR202528 Sequence
c 667	17	1.1	33	6	AX172816	AX172816 Sequence
668	17	1.1	35	6	A25417	A25417 oligonucleo
669	17	1.1	35	6	AR096977	AR096977 Sequence
c 670	17	1.1	35	6	AR145497	AR145497 Sequence
671	17	1.1	36	6	AX398700	AX398700 Sequence
c 672	17	1.1	37	6	AR093706	AR093706 Sequence
c 673	17	1.1	37	6	AR094473	AR094473 Sequence
c 674	17	1.1	37	6	AR139630	AR139630 Sequence
c 675	17	1.1	37	6	AR154142	AR154142 Sequence
676	17	1.1	38	6	AR016401	AR016401 Sequence
677	17	1.1	38	6	AR019259	AR019259 Sequence
c 678	17	1.1	38	6	AR058958	AR058958 Sequence
c 679	17	1.1	38	6	AR105232	AR105232 Sequence
c 680	17	1.1	38	6	AR119153	AR119153 Sequence
c 681	17	1.1	38	6	AR123524	AR123524 Sequence
c 682	17	1.1	38	6	AR138177	AR138177 Sequence
c 683	17	1.1	38	6	AR176738	AR176738 Sequence
c 684	17	1.1	38	6	AR198309	AR198309 Sequence
685	17	1.1	38	6	AX219129	AX219129 Sequence
686	17	1.1	38	6	AX273417	AX273417 Sequence
687	17	1.1	38	6	AX398684	AX398684 Sequence
688	17	1.1	38	6	AX398696	AX398696 Sequence
c 689	17	1.1	38	6	AX470002	AX470002 Sequence
690	17	1.1	39	6	AX108712	AX108712 Sequence
691	17	1.1	39	6	AX250381	AX250381 Sequence
692	17	1.1	39	6	AX306732	AX306732 Sequence
693	17	1.1	39	6	AX351191	AX351191 Sequence
694	17	1.1	39	6	AX351194	AX351194 Sequence
695	17	1.1	40	6	AR053704	AR053704 Sequence
c 696	17	1.1	40	6	AR201283	AR201283 Sequence
697	17	1.1	41	6	AR002620	AR002620 Sequence
698	17	1.1	41	6	AR099670	AR099670 Sequence
699	17	1.1	41	6	AX004833	AX004833 Sequence
700	17	1.1	41	6	AX004836	AX004836 Sequence
c 701	17	1.1	41	6	AX128372	AX128372 Sequence
702	17	1.1	41	6	AX190443	AX190443 Sequence
c 703	17	1.1	42	6	AR063931	AR063931 Sequence
c 704	17	1.1	42	6	AX236436	AX236436 Sequence
c 705	17	1.1	42	6	I92764	I92764 Sequence 30
c 706	17	1.1	43	6	AR200692	AR200692 Sequence
c 707	17	1.1	43	6	AX077423	AX077423 Sequence
c 708	17	1.1	43	6	AX097541	AX097541 Sequence
c 709	17	1.1	43	6	AX301891	AX301891 Sequence
710	17	1.1	44	6	AX027828	AX027828 Sequence
711	17	1.1	44	6	E11300	E11300 PCR primer
c 712	17	1.1	45	6	AR002619	AR002619 Sequence
c 713	17	1.1	45	6	AR099106	AR099106 Sequence
c 714	17	1.1	45	6	AR099669	AR099669 Sequence
715	17	1.1	45	6	AX068136	AX068136 Sequence
716	17	1.1	45	6	AX068137	AX068137 Sequence
717	17	1.1	45	6	AX068139	AX068139 Sequence
c 718	17	1.1	45	6	AX201011	AX201011 Sequence
c 719	17	1.1	45	6	AX267810	AX267810 Sequence.
c 720	17	1.1	46	6	A20001	A20001 SEQ ID NO:
c 721	17	1.1	46	6	A98768	A98768 Sequence 1
722	17	1.1	46	6	A98769	A98769 Sequence 2
723	17	1.1	46	6	AR032563	AR032563 Sequence
724	17	1.1	46	6	AR035242	AR035242 Sequence
725	17	1.1	46	6	AR209227	AR209227 Sequence
c 726	17	1.1	46	6	I13190	I13190 Sequence 10
727	17	1.1	46	6	I29303	I29303 Sequence 17
728	17	1.1	46	6	I90977	I90977 Sequence 17
c 729	17	1.1	47	6	AX136052	AX136052 Sequence
c 730	17	1.1	47	6	AX194988	AX194988 Sequence
c 731	17	1.1	47	6	AX195019	AX195019 Sequence
c 732	17	1.1	47	6	AX195025	AX195025 Sequence
c 733	17	1.1	47	6	AX278085	AX278085 Sequence
734	17	1.1	47	6	E13626	E13626 Polyribonuc
735	17	1.1	48	6	A38191	A38191 Sequence 35
736	17	1.1	48	6	AR127012	AR127012 Sequence
737	17	1.1	48	6	E13604	E13604 Linker. 4/1
738	17	1.1	48	10	MMC7RNA	X60868 M.musculus
739	17	1.1	49	6	A38192	A38192 Sequence 36
740	17	1.1	49	6	AX207722	AX207722 Sequence
741	17	1.1	49	6	AX279596	AX279596 Sequence
742	17	1.1	49	6	AX279607	AX279607 Sequence
743	17	1.1	49	6	AX279718	AX279718 Sequence
744	17	1.1	49	6	AX279764	AX279764 Sequence
745	17	1.1	49	6	AX391613	AX391613 Sequence
746	17	1.1	49	6	I21262	I21262 Sequence 26
c 747	17	1.1	50	6	AR032752	AR032752 Sequence
c 748	17	1.1	50	6	AR032885	AR032885 Sequence
c 749	17	1.1	50	6	AR182233	AR182233 Sequence
c 750	17	1.1	50	6	AR209416	AR209416 Sequence
c 751	17	1.1	50	6	AR209549	AR209549 Sequence
752	17	1.1	50	6	AX014758	AX014758 Sequence
c 753	17	1.1	50	6	AX162314	AX162314 Sequence
754	17	1.1	50	6	AX165809	AX165809 Sequence
755	17	1.1	50	6	AX199450	AX199450 Sequence
756	17	1.1	50	6	AX199516	AX199516 Sequence
c 757	17	1.1	50	6	AX279744	AX279744 Sequence
c 758	17	1.1	50	6	AX430850	AX430850 Sequence
c 759	17	1.1	50	6	I21272	I21272 Sequence 36
c 760	17	1.1	50	6	I29492	I29492 Sequence 36
c 761	17	1.1	50	6	I29625	I29625 Sequence 49
c 762	17	1.1	50	6	I91166	I91166 Sequence 36
c 763	17	1.1	50	6	I91299	I91299 Sequence 49
c 764	16.8	1.1	29	6	A52310	A52310 Sequence 14
c 765	16.8	1.1	29	6	AR050002	AR050002 Sequence
c 766	16.8	1.1	29	6	AR100031	AR100031 Sequence
767	16.8	1.1	30	6	AR081910	AR081910 Sequence
c 768	16.8	1.1	30	6	AR122637	AR122637 Sequence
c 769	16.8	1.1	30	6	AR164243	AR164243 Sequence
770	16.8	1.1	30	6	AR202765	AR202765 Sequence
771	16.8	1.1	30	6	E04646	E04646 Synthetic n
772	16.8	1.1	30	6	E04677	E04677 Synthetic n
c 773	16.8	1.1	30	6	E04677	E04677 Synthetic n
c 774	16.8	1.1	30	6	I49873	I49873 Sequence 64
775	16.8	1.1	31	6	AX248452	AX248452 Sequence
c 776	16.8	1.1	31	6	AX249447	AX249447 Sequence
777	16.8	1.1	31	6	BD002867	BD002867 Gene comp
c 778	16.8	1.1	33	6	A62639	A62639 Sequence 3
779	16.8	1.1	33	6	AR024310	AR024310 Sequence
c 780	16.8	1.1	33	6	AR024311	AR024311 Sequence
781	16.8	1.1	33	6	AR045163	AR045163 Sequence
c 782	16.8	1.1	33	6	AR045164	AR045164 Sequence
c 783	16.8	1.1	33	6	AR144717	AR144717 Sequence
c 784	16.8	1.1	33	6	AX406738	AX406738 Sequence
785	16.8	1.1	33	6	BD011387	BD011387 Chimeric
c 786	16.8	1.1	33	6	BD011388	BD011388 Chimeric
787	16.8	1.1	33	6	E43857	E43857 Chimeric an
c 788	16.8	1.1	33	6	E43858	E43858 Chimeric an
789	16.8	1.1	33	10	MMM1103	X94887 M.musculus
c 790	16.8	1.1	35	6	AX015342	AX015342 Sequence
791	16.8	1.1	35	6	BD002993	BD002993 A method
792	16.8	1.1	35	6	BD002995	BD002995 A method
793	16.8	1.1	36	6	AR051239	AR051239 Sequence
794	16.8	1.1	36	6	I28368	I28368 Sequence 7
795	16.8	1.1	36	6	I34917	I34917 Sequence 3

	796	16.8	1.1	37	6	AR012329
c	797	16.8	1.1	37	6	AR012354
	798	16.8	1.1	38	6	AX219810
	799	16.8	1.1	38	6	AX219868
	800	16.8	1.1	38	6	AX273741
	801	16.8	1.1	38	6	AX424420
	802	16.8	1.1	38	6	AX424439
	803	16.8	1.1	38	6	AX424482
	804	16.8	1.1	38	6	I05583
	805	16.8	1.1	39	6	AX167048
	806	16.8	1.1	39	6	AX167053
	807	16.8	1.1	40	6	AR079802
	808	16.8	1.1	40	6	AR081332
	809	16.8	1.1	40	6	AR170692
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c	940	16.6	1.1	36	6	AX080054
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	993	16.6	1.1	45	6	BD006045 BD006045 Polynucle
	994	16.6	1.1	45	9	HSTCCF24A Z49956 H.sapiens m
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ALIGNMENTS

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RESULT 1
AX146582/c
LOCUS       AX146582                  50 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 44 from Patent WO0134654.
ACCESSION   AX146582
VERSION     AX146582.1  GI:14284975
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Strauch,K.
  TITLE     Hedgehog fusion proteins and uses
  JOURNAL   Patent: WO 0134654-A 44 17-MAY-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       11 a      11 c      15 g      13 t
ORIGIN

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  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
AX146613/c
LOCUS       AX146613                  50 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 75 from Patent WO0134654.
ACCESSION   AX146613
VERSION     AX146613.1  GI:14285006
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Strauch,K.
  TITLE     Hedgehog fusion proteins and uses
  JOURNAL   Patent: WO 0134654-A 75 17-MAY-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches   49;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     228 CGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACCCCTTTA 277
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Db      50 CGGGCAGGGGGTTCGGGAAGAAGAGGCACCCCAAAAAGCTGACCCCTTTA 1


RESULT 3
AX146614/c
LOCUS       AX146614                  50 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 76 from Patent WO0134654.
ACCESSION   AX146614
VERSION     AX146614.1  GI:14285007
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Strauch,K.
  TITLE     Hedgehog fusion proteins and uses
  JOURNAL   Patent: WO 0134654-A 76 17-MAY-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
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BASE COUNT         6 a      19 c      13 g      12 t
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Qy     228 CGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACCCCTTTA 277
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Db      50 CGGGCAGGGGGTTCGGGAGGAGGAGGCACCCCAAAAAGCTGACCCCTTTA 1


RESULT 4
AX146616/c
LOCUS       AX146616                 50 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 78 from Patent WO0134654.
ACCESSION   AX146616
VERSION     AX146616.1  GI:14285009
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Strauch,K.
  TITLE     Hedgehog fusion proteins and uses
  JOURNAL   Patent: WO 0134654-A 78 17-MAY-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT         6 a      19 c      15 g      10 t
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Qy     228 CGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACCCCTTTA 277
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Db      50 CGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCCAGCAGCTGACCCCTTTA 1


RESULT 5
AX146608
LOCUS       AX146608                 47 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 70 from Patent WO0134654.
ACCESSION   AX146608
VERSION     AX146608.1  GI:14285001
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Strauch,K.
  TITLE     Hedgehog fusion proteins and uses
  JOURNAL   Patent: WO 0134654-A 70 17-MAY-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches   45;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     225 GACCGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACC 271
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RESULT 6
AX146609
LOCUS       AX146609                 47 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 71 from Patent WO0134654.
ACCESSION   AX146609
VERSION     AX146609.1  GI:14285002
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Strauch,K.
  TITLE     Hedgehog fusion proteins and uses
  JOURNAL   Patent: WO 0134654-A 71 17-MAY-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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BASE COUNT        11 a      13 c      20 g       3 t
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Qy     225 GACCGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACC 271
           | ||||||||||||||||||| |||||||||||||||||||||||||
Db       1 GCCCGGGCAGGGGGTTCGGGAGGAGGAGGCACCCCAAAAAGCTGACC 47


RESULT 7
AX146612
LOCUS       AX146612                 45 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 74 from Patent WO0134654.
ACCESSION   AX146612
VERSION     AX146612.1  GI:14285005
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Strauch,K.
  TITLE     Hedgehog fusion proteins and uses
  JOURNAL   Patent: WO 0134654-A 74 17-MAY-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        12 a      14 c      10 g       9 t
ORIGIN

  Query Match              2.8%;  Score 43.4;  DB 6;  Length 45;
  Best Local Similarity   97.8%;  Pred. No. 4.3e+04;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     272 CCTTTAGCCTACAAGCAGTTTATCCCCAATGTGGCCGAGAAGACC 316
           |||||||||||||||||||||||||||||| ||||||||||||||||
Db       1 CCTTTAGCCTACAAGCAGTTTATCCCCAAGGTGGCCGAGAAGACC 45


RESULT 8
AX146615/c
LOCUS       AX146615                 50 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 77 from Patent WO0134654.
```

```
ACCESSION   AX146615
VERSION     AX146615.1  GI:14285008
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Strauch,K.
  TITLE     Hedgehog fusion proteins and uses
  JOURNAL   Patent: WO 0134654-A 77 17-MAY-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        6 a     16 c     16 g     12 t
ORIGIN

  Query Match             2.7%;  Score 42;  DB 6;  Length 50;
  Best Local Similarity   90.0%;  Pred. No. 6.1e+04;
  Matches   45;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy     228 CGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACCCCTTTA 277
           |||||||||||||||||  ||   |  |||||||||||||||||||||||||
Db      50 CGGGCAGGGGGTTCGGGCAGCAGCAGCACCCCAAAAAGCTGACCCCTTTA 1


RESULT 9
AX146617/c
LOCUS       AX146617                  43 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 79 from Patent WO0134654.
ACCESSION   AX146617
VERSION     AX146617.1  GI:14285010
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Strauch,K.
  TITLE     Hedgehog fusion proteins and uses
  JOURNAL   Patent: WO 0134654-A 79 17-MAY-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        8 a     10 c     14 g     11 t
ORIGIN

  Query Match             2.6%;  Score 41.4;  DB 6;  Length 43;
  Best Local Similarity   97.7%;  Pred. No. 7.5e+04;
  Matches   42;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     278 GCCTACAAGCAGTTTATCCCCAATGTGGCCGAGAAGACCCTAG 320
           |||||||||||||||  |||||||||||||||||||||||||||
Db      43 GCCTACAAGCAGTTTCTCCCCAATGTGGCCGAGAAGACCCTAG 1


RESULT 10
AX146611
LOCUS       AX146611                  47 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 73 from Patent WO0134654.
ACCESSION   AX146611
VERSION     AX146611.1  GI:14285004
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Strauch,K.
  TITLE     Hedgehog fusion proteins and uses
  JOURNAL   Patent: WO 0134654-A 73 17-MAY-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        9 a     15 c     20 g      3 t
ORIGIN

  Query Match             2.6%;  Score 40.6;  DB 6;  Length 47;
  Best Local Similarity   91.5%;  Pred. No. 9.2e+04;
  Matches   43;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     225 GACCGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACC 271
           | |||||||||||||||||||||||||||||||||||| |  ||||||||
Db       1 GCCCGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCCAGCAGCTGACC 47


RESULT 11
AX146610
LOCUS       AX146610                  47 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 72 from Patent WO0134654.
ACCESSION   AX146610
VERSION     AX146610.1  GI:14285003
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Strauch,K.
  TITLE     Hedgehog fusion proteins and uses
  JOURNAL   Patent: WO 0134654-A 72 17-MAY-2001;
            BIOGEN, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       11 a     16 c     17 g      3 t
ORIGIN

  Query Match             2.4%;  Score 37.4;  DB 6;  Length 47;
  Best Local Similarity   87.2%;  Pred. No. 2.2e+05;
  Matches   41;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     225 GACCGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACC 271
           | ||||||||||||||||||  ||   |  ||||||||||||||||||
Db       1 GCCCGGGCAGGGGGTTCGGGCAGCAGCAGCACCCCAAAAAGCTGACC 47


RESULT 12
AX057285
LOCUS       AX057285                  50 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 16 from Patent WO0075329.
ACCESSION   AX057285
VERSION     AX057285.1  GI:12310031
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Levine,A.J., Mitterer,A., Falkner,F.G., Scheiflinger,F. and
            Dorner,F.
  TITLE     Targeted angiogenesis
  JOURNAL   Patent: WO 0075329-A 16 14-DEC-2000;
            Edwards Lifesciences Corporation (US) ; Baxter Aktiengesellschaft
            (AT)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="annealed oligonucleotide"
```

```
BASE COUNT        3 a     16 c     27 g      4 t
ORIGIN

  Query Match             2.0%;  Score 31.4;  DB 6;  Length 50;
  Best Local Similarity   85.4%;  Pred. No. 1.1e+06;
  Matches   35;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   1341 GCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGC 1381
          ||||||| | |||||||||||| | | |||| |||||||||
Db      7 GCGGCGGCGGCAGCGGCGGCGGCGGCAGCGGCGGCGGCGGC 47


RESULT 13
HSA270316/c
LOCUS       HSA270316                27 bp    DNA     linear   PRI 26-JUL-2000
DEFINITION  Homo sapiens sonic hedgehog (Drosophila) homolog (SHH) antisense
            primer.
ACCESSION   AJ270316
VERSION     AJ270316.1  GI:9557893
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Palm,K., Salin-Nordstrom,T., Levesque,M.F. and Neuman,T.
  TITLE     Fetal and adult human CNS stem cells have similar molecular
            characteristics and developmental potential
  JOURNAL   Brain Res. Mol. Brain Res. 78 (1-2), 192-195 (2000)
  MEDLINE   20351569
   PUBMED   10891600
REFERENCE   2  (bases 1 to 27)
  AUTHORS   Palm,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-OCT-1999) Surgery, Cedars Sinai Medical Center, 8700
            Beverly Blvd., Los Angeles, CA 90048, US
COMMENT     Related entry: NM_000193.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    1. .27
                     /note="PCR antisense primer for sonic hedgehog
                     (Drosophila) homolog (SHH)"
BASE COUNT        3 a     11 c      9 g      4 t
ORIGIN

  Query Match             1.7%;  Score 27;  DB 9;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+06;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    755 TCGGCCACGGTGCACCTGGAGCAGGGC 781
          |||||||||||||||||||||||||||
Db     27 TCGGCCACGGTGCACCTGGAGCAGGGC 1


RESULT 14
AR178318
LOCUS       AR178318                 50 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 35 from patent US 6319672.
ACCESSION   AR178318
VERSION     AR178318.1  GI:20219456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
  TITLE     Purification of a triple helix formation with an immobilized
            oligonucleotide
  JOURNAL   Patent: US 6319672-A 35 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       25 a      0 c     25 g      0 t
ORIGIN

  Query Match             1.6%;  Score 26;  DB 6;  Length 50;
  Best Local Similarity   70.0%;  Pred. No. 5e+06;
  Matches   35;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     19 GAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGA 68
          ||||||| ||| | | |||   ||| |||  || || || |  |||||||
Db      1 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 50


RESULT 15
AX323400
LOCUS       AX323400                 50 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 35 from Patent WO0192511.
ACCESSION   AX323400
VERSION     AX323400.1  GI:18094162
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
  TITLE     Purification of a triple helix formation with an immobilized
            oligonucleotide
  JOURNAL   Patent: WO 0192511-A 35 06-DEC-2001;
            Aventis Pharma (FR)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide"
BASE COUNT       25 a      0 c     25 g      0 t
ORIGIN

  Query Match             1.6%;  Score 26;  DB 6;  Length 50;
  Best Local Similarity   70.0%;  Pred. No. 5e+06;
  Matches   35;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     19 GAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGA 68
          ||||||| ||| | | |||   ||| |||  || || || |  |||||||
Db      1 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 50


RESULT 16
I84406
LOCUS       I84406                   33 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 7 from patent US 5695933.
ACCESSION   I84406
VERSION     I84406.1  GI:3021926
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Schalling,M., Hudson,T.J. and Housman,D.E.
  TITLE     Direct detection of expanded nucleotide repeats in the human genome
  JOURNAL   Patent: US 5695933-A 7 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        0 a     11 c     22 g      0 t
ORIGIN

  Query Match             1.6%;  Score 25;  DB 6;  Length 33;
  Best Local Similarity   84.8%;  Pred. No. 7.4e+06;
  Matches   28;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   1351 CAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGG 1383
          | |||||||||| | | |||| ||||||||||
Db      1 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 33
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RESULT 17
AR199385
LOCUS       AR199385                 50 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 6 from patent US 6355434.
ACCESSION   AR199385
VERSION     AR199385.1  GI:20249459
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Drazen,J.M., In,K.-H., Asano,K., Beier,D. and Grobholz,J.
  TITLE     5-Lipoxygenase gene polymorphisms and their use in classifying
            patients
  JOURNAL   Patent: US 6355434-A 6 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT        6 a     10 c     32 g      2 t
ORIGIN

  Query Match             1.6%;  Score 24.6;  DB 6;  Length 50;
  Best Local Similarity   76.9%;  Pred. No. 7.4e+06;
  Matches   30;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   1348 GGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCAG 1386
          | || |||| ||||||| | | || || ||||| |||||
Db      6 GTACTGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCAG 44


RESULT 18
AR063105
LOCUS       AR063105                 24 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 43 from patent US 5844079.
ACCESSION   AR063105
VERSION     AR063105.1  GI:5990796
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Ingham,P.W., McMahon,A.P. and Tabin,C.J.
  TITLE     Vertebrate embryonic pattern-inducing proteins, and uses related
            thereto
  JOURNAL   Patent: US 5844079-A 43 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      5 c     11 g      2 t
ORIGIN

  Query Match             1.5%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+07;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    524 ACCGAGGGCTGGGACGAAGATGGC 547
          ||||||||||||||||||||||||
Db      1 ACCGAGGGCTGGGACGAAGATGGC 24


RESULT 19
AR122632
LOCUS       AR122632                 24 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 43 from patent US 6165747.
ACCESSION   AR122632
VERSION     AR122632.1  GI:14106949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Ingham,P.W., McMahon,A.P., Tabin,C.J., Bumcrot,D.A. and
            Marti-Gorostiza,E.
  TITLE     Nucleic acids encoding hedgehog proteins
  JOURNAL   Patent: US 6165747-A 43 26-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      5 c     11 g      2 t
ORIGIN

  Query Match             1.5%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+07;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    524 ACCGAGGGCTGGGACGAAGATGGC 547
          ||||||||||||||||||||||||
Db      1 ACCGAGGGCTGGGACGAAGATGGC 24


RESULT 20
AR164260
LOCUS       AR164260                 24 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 43 from patent US 6271363.
ACCESSION   AR164260
VERSION     AR164260.1  GI:16235331
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Ingham,P.W., McMahon,A.P. and Tabin,C.J.
  TITLE     Nucleic acids encoding hedgehog proteins
  JOURNAL   Patent: US 6271363-A 43 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      5 c     11 g      2 t
ORIGIN

  Query Match             1.5%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+07;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    524 ACCGAGGGCTGGGACGAAGATGGC 547
          ||||||||||||||||||||||||
Db      1 ACCGAGGGCTGGGACGAAGATGGC 24


RESULT 21
AR208932
LOCUS       AR208932                 24 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 43 from patent US 6384192.
ACCESSION   AR208932
VERSION     AR208932.1  GI:21510216
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Ingham,P.W., McMahon,A.P. and Tabin,C.J.
  TITLE     Vertebrate embryonic pattern-inducing proteins
  JOURNAL   Patent: US 6384192-A 43 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      5 c     11 g      2 t
ORIGIN

  Query Match             1.5%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+07;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    524 ACCGAGGGCTGGGACGAAGATGGC 547
```

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              ||||||||||||||||||||||||
Db        1 ACCGAGGGCTGGGACGAAGATGGC 24


RESULT 22
I20760
LOCUS       I20760                    45 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 13 from patent US 5516637.
ACCESSION   I20760
VERSION     I20760.1  GI:1601115
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Huang,G.P., Rhode,P.R., Stinson,J.R. and Wong,H.C.
  TITLE     Method involving display of protein binding pairs on the surface of
            bacterial pili and bacteriophage
  JOURNAL   Patent: US 5516637-A 13 14-MAY-1996;
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="unknown"
BASE COUNT        2 a      9 c     25 g      9 t
ORIGIN

  Query Match             1.5%;  Score 24;  DB 6;  Length 45;
  Best Local Similarity   75.0%;  Pred. No. 8.9e+06;
  Matches   30;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy   1341 GCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGG 1380
           | ||||| | ||||||||| || |    ||| ||||||||
Db      2 GTGGCGGTGGCAGCGGCGGTGGTGGTTCCGGAGGCGGCGG 41


RESULT 23
I84401/c
LOCUS       I84401                    30 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 2 from patent US 5695933.
ACCESSION   I84401
VERSION     I84401.1  GI:3021921
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Schalling,M., Hudson,T.J. and Housman,D.E.
  TITLE     Direct detection of expanded nucleotide repeats in the human genome
  JOURNAL   Patent: US 5695933-A 2 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
BASE COUNT        0 a      20 c     10 g      0 t
ORIGIN

  Query Match             1.5%;  Score 23.6;  DB 6;  Length 30;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+07;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1354 CGGCGGCGGGGACCGCGGGGGCGGCGGCGG 1383
           ||||||||| | | |||| ||||||||||
Db     30 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1


RESULT 24
A01419/c
LOCUS       A01419                    31 bp    DNA     linear   PAT 28-APR-1993
DEFINITION  Malaria parasitic epitope (T-cell).
ACCESSION   A01419
VERSION     A01419.1  GI:344347
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        0 a      20 c     10 g      0 t      1 others
ORIGIN

  Query Match             1.5%;  Score 23.6;  DB 6;  Length 31;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+07;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1355 GGCGGCGGGGACCGCGGGGGCGGCGGCGGC 1384
           |||||||| | | |||| ||||||||||||
Db     30 GGCGGCGGCGGCGGCGGCGGCGGCGGCGGC 1


RESULT 25
A62993/c
LOCUS       A62993                    32 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 5 from Patent WO9720068.
ACCESSION   A62993
VERSION     A62993.1  GI:3716865
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Oerum,H. and Seeger,C.
  TITLE     METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
  JOURNAL   Patent: WO 9720068-A 5 05-JUN-1997;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        0 a      30 c      2 g      0 t
ORIGIN

  Query Match             1.4%;  Score 22.4;  DB 6;  Length 32;
  Best Local Similarity   81.2%;  Pred. No. 1.5e+07;
  Matches   26;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   1543 CCGGGGGGCCGGGGGAGGGGCGCGGGAGGGGG 1574
           ||||||||  ||||| |||| | ||| |||||
Db     32 CCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1


Search completed: March 13, 2003, 23:14:50
Job time : 4408 secs
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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 13, 2003, 20:47:37 ; Search time 395 Seconds
(without alignments)
8985.188 Million cell updates/sec

Title: US-10-001-844-3
Perfect score: 1576
Sequence: 1 gcgaggcagccagcgaggga.....gaggggcgcgggaggggcc 1576

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	50	3.2	50	22	AAD09047	Human oligonucleot
c	2	48.4	3.1	50	22	AAD09078	Human oligonucleot
c	3	48.4	3.1	50	22	AAD09079	Human oligonucleot
c	4	45.2	2.9	50	22	AAD09081	Human oligonucleot
	5	43.8	2.8	47	22	AAD09073	Human oligonucleot
	6	43.8	2.8	47	22	AAD09074	Human oligonucleot
	7	43.4	2.8	45	22	AAD09077	Human oligonucleot
c	8	43.2	2.7	48	22	AAF27031	Human Sonic hedgeh
c	9	43.2	2.7	48	22	AAF27034	Human Sonic hedgeh
c	10	42	2.7	50	22	AAD09080	Human oligonucleot
c	11	41.4	2.6	43	22	AAD09082	Human oligonucleot
	12	40.6	2.6	47	22	AAD09076	Human oligonucleot
	13	37.4	2.4	47	22	AAD09075	Human oligonucleot
c	14	37.2	2.4	42	22	AAF27032	Human Sonic hedgeh
c	15	37.2	2.4	42	22	AAF27036	Human Sonic hedgeh
c	16	36.4	2.3	38	22	AAF27039	Human Sonic hedgeh
c	17	36	2.3	49	22	AAF27025	Human Sonic hedgeh
c	18	35.8	2.3	39	22	AAF27038	Human Sonic hedgeh
c	19	35.6	2.3	42	22	AAF27035	Human Sonic hedgeh
c	20	33.8	2.1	37	22	AAF27037	Human Sonic hedgeh
c	21	33.4	2.1	35	22	AAF27041	Human Sonic hedgeh
c	22	32.2	2.0	37	22	AAF27040	Human Sonic hedgeh
c	23	27	1.7	27	24	ABT03768	Human SHH gene PCR
	24	26.8	1.7	46	13	AAQ33571	Microsatellite seq
	25	26.4	1.7	45	22	AAF60024	DNA linker. Synth
	26	26	1.6	50	24	AAS21107	(GA)25 DNA purific
	27	25.6	1.6	50	22	AAL29061	Human SNP oligonuc
	28	25	1.6	33	15	AAQ73441	Crohn's disease/ul
c	29	24.4	1.5	49	15	AAQ79189	Plasmodium falcipa
	30	24	1.5	24	16	AAQ91654	Human sonic hedgeh
	31	24	1.5	24	19	AAV18405	Human mutated soni
	32	24	1.5	24	22	AAH76132	Human Shh DNA ampl
	33	24	1.5	24	22	AAD10171	Human Sonic hedgeh
	34	24	1.5	24	22	AAC87097	PCR primer for cDN
	35	24	1.5	24	24	ABN87569	Human sonic hedgeh
	36	24	1.5	45	19	AAV54346	Modified pel B lea
	37	24	1.5	45	20	AAX55429	Primer to amplify
	38	24	1.5	48	13	AAQ33615	Microsatellite seq
	39	23.6	1.5	38	22	AAD14353	Human manganese su
	40	23.6	1.5	48	21	AAC60679	Triplet repeat blo
c	41	23.4	1.5	25	19	AAV18406	Human mutated soni
	42	23.4	1.5	33	19	AAV62418	Human Sonic hedgeh
	43	23.4	1.5	49	13	AAQ33523	Sequence of micros
c	44	22.8	1.4	50	22	AAL28997	Human SNP oligonuc
c	45	22.6	1.4	50	21	AAC26760	Human secreted pro
c	46	22.4	1.4	32	24	ABK10414	Synthetic primer s
	47	22.2	1.4	36	13	AAQ28347	bGH N-terminus fra
	48	22.2	1.4	44	13	AAQ33577	Microsatellite seq
c	49	22.2	1.4	50	24	ABK47920	Vector multiclonin
	50	22	1.4	24	24	ABT03767	Human SHH gene PCR
c	51	22	1.4	29	21	AAA28861	Oligo linker for c
c	52	22	1.4	29	22	AAD09042	Human oligonucleot
c	53	22	1.4	29	24	AAK99702	Human sonic hedgeh
	54	22	1.4	47	22	AAF27024	Human Sonic hedgeh
c	55	22	1.4	50	22	AAF27026	Human Sonic hedgeh
	56	21.8	1.4	50	22	AAL34112	Human SNP oligonuc
c	57	21.8	1.4	50	22	AAL34422	Human SNP oligonuc
	58	21.6	1.4	40	20	AAX08533	Oligonucleotide fr
c	59	21.6	1.4	50	24	ABK94536	Human BRCA1 gene,
	60	21.4	1.4	24	24	AAD34564	Shh specific forwa
c	61	21.4	1.4	31	24	ABK10413	Synthetic primer s
	62	21.4	1.4	45	21	AAA37204	Human PRO1347 hybr
	63	21.4	1.4	45	22	AAF54306	Probe #23 used in
	64	21.4	1.4	49	18	AAT80502	Hepatoma AS-30D Ty
	65	21.4	1.4	50	21	AAA76957	Human clone cg4265
	66	21.2	1.3	41	24	AAK99303	Human cancer suppr
	67	21.2	1.3	41	24	AAK99304	Human cancer suppr
c	68	21.2	1.3	45	24	ABK94442	Human BRCA1/hMLH1
	69	21.2	1.3	49	24	ABK47921	Vector multiclonin
	70	21.2	1.3	50	16	AAQ89058	VEGF 2'-NH2-RNA nu
	71	21.2	1.3	50	22	AAL30005	Human SNP oligonuc
c	72	21.2	1.3	50	22	AAL34654	Human SNP oligonuc
c	73	21.2	1.3	50	24	ABK94441	Human BRCA1 gene,
c	74	21	1.3	40	17	AAT03676	Hepatitis C diagno
	75	21	1.3	48	12	AAQ14203	Probe P1674 for Gi
	76	21	1.3	48	13	AAQ28517	Hypercalcaemia age
c	77	21	1.3	50	15	AAQ69624	Human bcl-2 proto-
c	78	21	1.3	50	18	AAV76464	Staphylococcus aur
c	79	21	1.3	50	18	AAT64086	Human B-cell leuke
c	80	21	1.3	50	20	AAX17374	Test sequence from
c	81	21	1.3	50	22	AAL29166	Human SNP oligonuc
	82	21	1.3	50	22	AAL31203	Human SNP oligonuc

c	83	21	1.3	50	22	AAH89771	Human coding sequ
c	84	21	1.3	50	24	ABK82865	DNA binding molecu
c	85	20.8	1.3	40	24	ABK94443	Human BRCA1/hMLH1
	86	20.8	1.3	43	20	AAV80298	DNA encoding pepti
	87	20.8	1.3	46	19	AAV10422	CAT gene 5'-end an
c	88	20.8	1.3	46	19	AAV10422	CAT gene 5'-end an
	89	20.8	1.3	49	23	ABA10869	Tail adaptor oligo
c	90	20.8	1.3	50	17	AAT28823	PCR primer for HTR
	91	20.8	1.3	50	22	AAL31522	Human SNP oligonuc
	92	20.8	1.3	50	22	AAH89754	Human coding sequ
c	93	20.6	1.3	38	22	AAH46872	B. napus turgor ge
c	94	20.6	1.3	45	21	AAC60682	Triplet repeat blo
	95	20.6	1.3	45	22	AAD04017	Synthetic linker D
	96	20.6	1.3	48	17	AAT06969	DNA encoding GM-CS
	97	20.6	1.3	49	18	AAT80501	Hepatoma AS-30D Ty
c	98	20.6	1.3	50	22	AAL28264	Human SNP oligonuc
c	99	20.6	1.3	50	22	AAI74261	Human silent SNP c
c	100	20.4	1.3	30	22	AAF99890	Immunostimulatory
c	101	20.4	1.3	30	24	ABK10411	Synthetic primer s
	102	20.4	1.3	30	24	ABK10417	Synthetic primer s
c	103	20.4	1.3	31	24	ABK87619	MALDI-TOF-MS analy
c	104	20.4	1.3	34	13	AAQ33761	Microsatellite seq
c	105	20.4	1.3	35	22	AAF99571	Immunostimulatory
c	106	20.4	1.3	35	24	ABL38795	Immunostimulatory
	107	20.4	1.3	40	18	AAT78196	Micro gene random
c	108	20.4	1.3	40	24	ABL41767	PCR primer used to
	109	20.4	1.3	41	16	AAQ89389	COX-2 oligonucleot
c	110	20.4	1.3	47	16	AAT05461	I-domain PCR prime
	111	20.4	1.3	49	18	AAT61251	Human antibody kap
c	112	20.4	1.3	49	23	ABA10851	Tail adaptor oligo
	113	20.4	1.3	50	18	AAV79438	Staphylococcus aur
	114	20.4	1.3	50	21	AAA38175	Primer used in ste
	115	20.4	1.3	50	22	AAL27861	Human SNP oligonuc
c	116	20.4	1.3	50	22	AAL34421	Human SNP oligonuc
	117	20.2	1.3	36	24	ABK15487	Urokinase plasmino
c	118	20.2	1.3	40	14	AAQ50877	HSV2 primer. Synt
	119	20.2	1.3	42	20	AAX35839	Antisense oligonuc
	120	20.2	1.3	46	15	AAQ69335	Human transmembran
	121	20.2	1.3	46	18	AAT63797	Human transmembran
	122	20.2	1.3	46	19	AAV10421	CAT gene 5'-end an
c	123	20.2	1.3	46	19	AAV10421	CAT gene 5'-end an
	124	20.2	1.3	46	20	AAX17085	Test sequence from
	125	20.2	1.3	46	24	ABK82576	DNA binding molecu
	126	20.2	1.3	48	20	AAX89502	PCR primer CIPCBD.
	127	20.2	1.3	48	20	AAZ31580	PCR primer for C.
c	128	20.2	1.3	49	22	AAL28471	Human SNP oligonuc
	129	20.2	1.3	50	20	AAX99195	M. avium 16S rRNA
c	130	20.2	1.3	50	22	AAL28814	Human SNP oligonuc
c	131	20.2	1.3	50	22	AAL29448	Human SNP oligonuc
c	132	20.2	1.3	50	22	AAL29798	Human SNP oligonuc
c	133	20.2	1.3	50	22	AAL29802	Human SNP oligonuc
	134	20	1.3	20	22	AAF87045	PCR primer for Shh
c	135	20	1.3	32	19	AAV62419	Human Sonic hedgeh
	136	20	1.3	36	13	AAQ33540	Microsatellite seq
	137	20	1.3	36	13	AAQ33597	Microsatellite seq
c	138	20	1.3	38	23	AAS13726	Simple sequence re
c	139	20	1.3	38	24	AAL45123	Oligonucleotide sy
c	140	20	1.3	42	20	AAX35839	Antisense oligonuc
	141	20	1.3	45	14	AAQ34598	Antisense probe fo
	142	20	1.3	45	21	AAC81272	Human/mouse histon
	143	20	1.3	45	21	AAC58253	Human PRO943 hybri
	144	20	1.3	45	21	AAZ65162	Probe specific for
	145	20	1.3	45	22	AAF44319	Human PRO943 hybri
	146	20	1.3	45	24	ABK11755	PRO943 cDNA specif
	147	20	1.3	45	24	ABK28594	Human PRO943 hybri
c	148	20	1.3	47	22	AAS13006	Optimal zinc bindi
	149	20	1.3	48	12	AAQ11624	Probe S3 complemen
c	150	20	1.3	50	18	AAT50946	Endoglycoceramidas
	151	19.8	1.3	38	12	AAQ13203	SP1X2S oligonucleo
	152	19.8	1.3	39	18	AAT87242	IL-4 2'NH2 RNA lig
	153	19.8	1.3	39	18	AAT87238	IL-4 2'NH2 RNA lig
	154	19.8	1.3	39	18	AAT87247	IL-4 2'NH2 RNA lig
	155	19.8	1.3	39	18	AAT87229	IL-4 2'NH2 RNA lig
c	156	19.8	1.3	40	13	AAQ25025	Anti-sense oligonu
	157	19.8	1.3	47	21	AAZ67690	Human map-related
	158	19.8	1.3	47	21	AAZ68205	Human map-related
c	159	19.8	1.3	47	23	AAH88364	CNS disorder-relat
	160	19.8	1.3	48	24	ABQ75860	Plasmid pFab sfiIL
c	161	19.8	1.3	50	22	AAL28998	Human SNP oligonuc
	162	19.8	1.3	50	22	AAD19759	Human granulocyte
c	163	19.6	1.2	45	21	AAA47006	PCR primer for DNA
	164	19.6	1.2	46	21	AAZ98490	H. discus derived
	165	19.6	1.2	47	15	AAQ68336	Diabody mutagenesi
c	166	19.6	1.2	48	22	AAD13086	Oligo DEVD-2 for c
	167	19.6	1.2	48	24	ABK97936	DNA encoding IFN-C
c	168	19.6	1.2	50	18	AAT73782	Multiplex short-PC
c	169	19.4	1.2	36	20	AAX79322	Human Lymphocytic
c	170	19.4	1.2	37	23	AAH77140	DRA adapter 2 olig
	171	19.4	1.2	39	12	AAQ12191	Probe derived from
	172	19.4	1.2	39	22	AAF27023	Human Sonic hedgeh
	173	19.4	1.2	43	18	AAT78827	Gamma heavy chain
	174	19.4	1.2	43	19	AAV39268	Primer O-529 used
	175	19.4	1.2	43	20	AAZ22022	Oligonucleotide us
	176	19.4	1.2	45	16	AAQ99068	(Ser4Gly)2 linker
	177	19.4	1.2	45	21	AAA12866	DNA encoding (Ser4
	178	19.4	1.2	46	22	AAF76771	Thermus terminator
	179	19.4	1.2	48	17	AAT06971	DNA encoding GM-CS
	180	19.4	1.2	49	22	AAI74185	Human silent SNP c
	181	19.4	1.2	50	22	AAL29423	Human SNP oligonuc
	182	19.4	1.2	50	22	AAL33811	Human SNP oligonuc
	183	19.4	1.2	50	22	AAD11599	Non-target oligo h
	184	19.2	1.2	24	21	AAA27226	Forward PCR primer
	185	19.2	1.2	24	21	AAA30347	Sonic hedgehog mRN
c	186	19.2	1.2	24	23	AAS13720	Simple sequence re
	187	19.2	1.2	24	24	AAI67720	Receptor Shh cDNA
	188	19.2	1.2	33	22	AAS44168	Neisseria meningit
c	189	19.2	1.2	36	9	AAN80523	Synthetic oligonuc
	190	19.2	1.2	36	14	AAQ43268	Sequence of mPC1 p
	191	19.2	1.2	36	24	ABK15479	Urokinase plasmino
	192	19.2	1.2	40	21	AAZ96043	Polynucleotide seq
c	193	19.2	1.2	40	21	AAZ96156	Polynucleotide seq
c	194	19.2	1.2	41	13	AAQ33801	Microsatellite seq
	195	19.2	1.2	41	19	AAV37415	Oligonucleotide se
c	196	19.2	1.2	41	24	ABL40950	Slicing factor Prp
	197	19.2	1.2	41	24	ABA05600	Human ribosomal pr
	198	19.2	1.2	41	24	ABA05601	Human ribosomal pr
	199	19.2	1.2	42	24	ABL54014	Primer for 3' end
	200	19.2	1.2	44	18	AAT65793	Repeat sequence fr
	201	19.2	1.2	45	15	AAQ70687	Purine rich region
c	202	19.2	1.2	45	15	AAQ70687	Purine rich region
c	203	19.2	1.2	45	21	AAA05784	Streptavidin displ
c	204	19.2	1.2	45	22	AAF67664	Xenopus insulator
	205	19.2	1.2	46	19	AAV33368	Nucleotide sequenc
c	206	19.2	1.2	47	15	AAQ63171	Primer for alpha 1
c	207	19.2	1.2	47	22	AAF24211	Human alpha-1 adre
	208	19.2	1.2	48	23	ABK07442	Human NOGO Amberzy
c	209	19.2	1.2	49	15	AAQ69655	Human adenosine de
c	210	19.2	1.2	49	18	AAT64117	Human adenosine de
c	211	19.2	1.2	49	20	AAX17405	Test sequence from
c	212	19.2	1.2	49	22	AAH50317	Bacterial 23S/5S R
c	213	19.2	1.2	49	24	ABK82896	DNA binding molecu
	214	19.2	1.2	50	20	AAX99196	M. fortuitum 16S r
	215	19.2	1.2	50	20	AAX99197	M. sorofulaceum 16
	216	19.2	1.2	50	20	AAX99198	M. smegmatis 16S r
	217	19.2	1.2	50	22	AAL33643	Human SNP oligonuc
c	218	19.2	1.2	50	22	AAL33814	Human SNP oligonuc
c	219	19.2	1.2	50	22	AAL33875	Human SNP oligonuc
c	220	19.2	1.2	50	22	AAL34564	Human SNP oligonuc
c	221	19.2	1.2	50	22	AAI77023	Human silent SNP c
	222	19.2	1.2	50	24	AAS17229	DNA sequence #2 fr
c	223	19	1.2	19	19	AAV18410	Human mutated soni
c	224	19	1.2	19	19	AAV18416	Human mutated soni
	225	19	1.2	19	22	AAH45473	PCR primer Shh-U2
	226	19	1.2	19	22	AAH45477	PCR primer Shh-U1
c	227	19	1.2	30	19	AAV54229	Primer KC118 used
c	228	19	1.2	30	19	AAV54231	Primer KC120 used

c	229	19	1.2	30	20	AAX55311
c	230	19	1.2	30	20	AAX55313
	231	19	1.2	30	21	AAA28860
	232	19	1.2	30	22	AAD09041
	233	19	1.2	30	24	AAK99701
	234	19	1.2	35	23	ABA95454
c	235	19	1.2	36	20	AAZ28440
	236	19	1.2	36	24	AAD39387
	237	19	1.2	38	17	AAT13180
	238	19	1.2	39	22	AAF25074
	239	19	1.2	39	22	AAF91516
	240	19	1.2	39	24	ABK37899
c	241	19	1.2	40	13	AAQ25017
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c	243	19	1.2	41	17	AAT38659
c	244	19	1.2	42	24	ABL54013
	245	19	1.2	43	22	AAS07342
	246	19	1.2	44	17	AAT33024
	247	19	1.2	44	19	AAV68379
	248	19	1.2	44	20	AAX77428
	249	19	1.2	44	21	AAC96956
	250	19	1.2	45	16	AAT04813
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	253	19	1.2	45	22	AAI79904
	254	19	1.2	46	15	AAQ68290
	255	19	1.2	47	20	AAX56654
	256	19	1.2	48	22	AAD06907
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	259	19	1.2	50	22	AAL30665
	260	19	1.2	50	22	AAL30666
	261	19	1.2	50	22	AAL31601
c	262	19	1.2	50	22	AAL33627
c	263	19	1.2	50	22	AAL33628
	264	18.8	1.2	31	22	AAI30620
c	265	18.8	1.2	32	22	AAF24860
	266	18.8	1.2	34	11	AAQ05011
	267	18.8	1.2	34	14	AAQ36325
	268	18.8	1.2	34	14	AAQ36326
	269	18.8	1.2	38	19	AAV31478
	270	18.8	1.2	38	21	AAZ37860
c	271	18.8	1.2	39	22	AAF25074
c	272	18.8	1.2	39	22	AAF74379
	273	18.8	1.2	40	20	AAV64755
	274	18.8	1.2	40	21	AAZ96151
	275	18.8	1.2	40	22	AAH24767
c	276	18.8	1.2	40	23	AAH77135
	277	18.8	1.2	41	15	AAQ62419
	278	18.8	1.2	41	24	ABL41574
c	279	18.8	1.2	42	18	AAT47461
c	280	18.8	1.2	42	21	AAA05761
	281	18.8	1.2	42	23	AAH77126
	282	18.8	1.2	43	16	AAQ81075
	283	18.8	1.2	43	18	AAT70014
	284	18.8	1.2	43	19	AAV31116
	285	18.8	1.2	43	21	AAZ44243
	286	18.8	1.2	44	16	AAQ83198
	287	18.8	1.2	45	12	AAQ11829
c	288	18.8	1.2	45	22	AAF67665
c	289	18.8	1.2	45	22	AAF67666
c	290	18.8	1.2	45	22	AAF67668
c	291	18.8	1.2	47	20	AAV64736
c	292	18.8	1.2	47	22	AAH24748
	293	18.8	1.2	48	15	AAQ54639
	294	18.8	1.2	48	18	AAT97589
	295	18.8	1.2	48	21	AAZ36788
	296	18.8	1.2	48	23	ABA09828
	297	18.8	1.2	48	23	ABA10959
	298	18.8	1.2	49	23	ABA10699
	299	18.8	1.2	49	23	ABA10720
	300	18.8	1.2	49	23	ABA10868
c	301	18.8	1.2	50	20	AAX52199

Soluble sc-TCR fus
Soluble sc-TCR fus
Oligo linker for c
Human oligonucleot
Human sonic hedgeh
Thermus thermophil
Primer 345, for am
Human PDE7A1 3' UT
Human insulin codi
Nucleotide sequenc
Plasmid pGemT-tbpB
Promoter replaceme
Sense oligonucleot
Human antibody ONS
Chimaeric human/mu
Primer for 5' end
Plasmid pVAC-1stc
Antibody H chain V
Clone #5 fragment
PCR primer VH1aF5.
PCR primer VH1aF5
B.stearothermophil
T-cell receptor V-
Soluble sc-TCR fus
Mutant preproricin
Diabody MAK195 pri
Primer 27. Synthe
Human oligo 14 to
Multiplex short-PC
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human single nucle
PCR primer for cDN
Sequence binding t
NGFR5par, targette
NGFR5anti, targett
PCR primer HSU4598
Crossover junction
Nucleotide sequenc
Pig3 response elem
HIV anti-viral oli
Polynucleotide seq
Nucleotide sequenc
DRA adapter 1 olig
Vector pVAC1 const
Probe #2 relating
Foldback triplex f
Human growth hormo
HLA adapter oligon
supF gene triplex
Triplex-forming ol
H chain variable r
Murine CD4/CD34 re
Synthetic nucleoti
Probe to minisatel
Xenopus insulator
Xenopus insulator
Xenopus insulator
HIV anti-viral oli
Nucleotide sequenc
Probe 679 to A1 ad
Shigella flexneri
PCR primer used to
Primer #9 from pri
Tail adaptor oligo
Tail adaptor oligo
Tail adaptor oligo
Tail adaptor oligo
Synthetic plasmid

c	302	18.8	1.2	50	21	AAA53010
c	303	18.8	1.2	50	22	AAL28815
c	304	18.8	1.2	50	22	AAL29447
c	305	18.8	1.2	50	22	AAL29797
c	306	18.8	1.2	50	22	AAL29801
c	307	18.8	1.2	50	22	AAL33727
c	308	18.8	1.2	50	22	AAL34059
	309	18.8	1.2	50	22	AAL34589
	310	18.8	1.2	50	24	ABQ72370
	311	18.6	1.2	25	15	AAQ55856
	312	18.6	1.2	25	16	AAQ85271
	313	18.6	1.2	25	20	AAX05267
c	314	18.6	1.2	28	20	AAZ11432
	315	18.6	1.2	28	21	AAZ43855
c	316	18.6	1.2	34	24	ABL56849
	317	18.6	1.2	36	22	AAF23429
	318	18.6	1.2	38	14	AAQ47082
	319	18.6	1.2	38	22	AAF28348
	320	18.6	1.2	40	22	AAS11890
	321	18.6	1.2	42	13	AAQ33587
	322	18.6	1.2	43	22	AAF25888
c	323	18.6	1.2	43	22	AAC86366
	324	18.6	1.2	44	17	AAT33029
	325	18.6	1.2	44	20	AAX78848
	326	18.6	1.2	44	20	AAX77433
	327	18.6	1.2	44	21	AAC96961
	328	18.6	1.2	45	20	AAX52474
	329	18.6	1.2	45	21	AAC81274
c	330	18.6	1.2	45	21	AAC58253
	331	18.6	1.2	45	21	AAC58432
c	332	18.6	1.2	45	21	AAZ65162
	333	18.6	1.2	45	22	AAF30752
c	334	18.6	1.2	45	22	AAF30753
	335	18.6	1.2	45	22	AAF72632
c	336	18.6	1.2	45	22	AAF44319
c	337	18.6	1.2	45	24	ABK11755
c	338	18.6	1.2	45	24	ABK28594
c	339	18.6	1.2	46	15	AAQ80661
c	340	18.6	1.2	46	20	AAX25415
	341	18.6	1.2	47	13	AAQ30484
	342	18.6	1.2	47	20	AAX55789
	343	18.6	1.2	48	22	AAD13085
c	344	18.6	1.2	49	21	AAC69816
c	345	18.6	1.2	49	23	ABA09825
	346	18.6	1.2	49	23	ABA10719
c	347	18.6	1.2	49	23	ABA10989
c	348	18.6	1.2	50	15	AAQ69713
c	349	18.6	1.2	50	18	AAT73798
c	350	18.6	1.2	50	18	AAT64175
c	351	18.6	1.2	50	19	AAV49719
	352	18.6	1.2	50	20	AAX99193
	353	18.6	1.2	50	20	AAX99194
	354	18.6	1.2	50	20	AAX52139
c	355	18.6	1.2	50	20	AAX17463
c	356	18.6	1.2	50	21	AAA76763
	357	18.6	1.2	50	22	AAL28867
c	358	18.6	1.2	50	22	AAL29985
	359	18.6	1.2	50	22	AAL31975
	360	18.6	1.2	50	22	AAL32200
c	361	18.6	1.2	50	22	AAL33786
c	362	18.6	1.2	50	22	AAL34150
	363	18.6	1.2	50	22	AAL34161
	364	18.6	1.2	50	22	AAL34195
	365	18.6	1.2	50	22	AAL34645
c	366	18.6	1.2	50	22	AAI73792
c	367	18.6	1.2	50	24	ABK82954
	368	18.4	1.2	20	19	AAV62410
c	369	18.4	1.2	20	22	AAF87046
c	370	18.4	1.2	28	22	AAF99570
c	371	18.4	1.2	28	24	ABL38794
c	372	18.4	1.2	33	20	AAX55438
c	373	18.4	1.2	33	21	AAZ94979
	374	18.4	1.2	33	22	AAF67671

Aspergillus niger
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
PCR primer MHV-Bac
Fragile X probe.
Probe for Fragile
Fragile X chromoso
Synthetic PGK prom
Human IgG4 heavy c
Peptide vector des
Reverse PCR primer
HIV ENV gene PCR p
Streptomyces livid
Monoscaffold antib
Downstream sequenc
Primer #2 used in
Linker used to mak
Antibody H chain V
Paraquat binding a
PCR primer VH4cF5.
PCR primer VH4cF5
Probe used to iso
Human/mouse histon
Human PRO943 hybri
Human PRO332 (UNQ2
Probe specific for
Rat brain factor-1
Rat brain factor-1
Human PRO polypept
Human PRO943 hybri
PRO943 cDNA specif
Human PRO943 hybri
CC49 V-light prime
Anti-TAG-72 MAb CC
Oligonucleotide co
Stable cruciform m
Oligo DEVD-1 for c
E. coli ebgR SELEX
Primer #6 from pri
Tail adaptor oligo
Tail adaptor oligo
Human insulin-like
Multiplex short-PC
Human insulin-like
Plasmid pSLHirKR1
M. tuberculosis 16
M. bovis 16S rRNA
Synthetic plasmid
Test sequence from
Human clone cg3212
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human SNP oligonuc
Human silent SNP c
DNA binding molecu
Human Desert hedge
PCR primer for Shh
Immunostimulatory
Immunostimulatory
Soluble sc-TCR fus
Primer KC176 used
Chicken insulator

	375	18.4	1.2	36	24	AAL39105	Antibody screening
	376	18.4	1.2	36	24	AAL39118	Antibody screening
c	377	18.4	1.2	39	21	AAZ94974	Primer JSS33(B) us
c	378	18.4	1.2	40	13	AAQ25030	Oligonucleotide sp
c	379	18.4	1.2	40	13	AAQ25029	Oligonucleotide sp
	380	18.4	1.2	40	21	AAZ96048	Polynucleotide seq
c	381	18.4	1.2	41	19	AAV51224	Maize polymorphic
	382	18.4	1.2	44	19	AAV11503	A. niger transposa
	383	18.4	1.2	44	21	AAZ34476	E. coli formate de
	384	18.4	1.2	44	22	AAC87576	E. coli fdh seleno
	385	18.4	1.2	45	17	AAT42435	GD domain region f
	386	18.4	1.2	45	20	AAX80091	Human PRO347 probe
	387	18.4	1.2	45	21	AAA46921	Probe used to scre
	388	18.4	1.2	45	21	AAA49497	Probe for cDNA enc
	389	18.4	1.2	45	21	AAZ36382	PCR primer DP47baN
	390	18.4	1.2	45	22	AAD16117	Human scFv gene VH
	391	18.4	1.2	45	24	ABK11184	DNA encoding Bipla
	392	18.4	1.2	45	24	ABA82885	Human protective D
	393	18.4	1.2	47	19	AAV49716	Plasmid pSLHirK1 o
c	394	18.4	1.2	47	19	AAV49717	Plasmid pSLHirK1 o
c	395	18.4	1.2	47	22	AAH26376	Mollusc acetylchol
	396	18.4	1.2	47	24	AAI72452	C7 coding region p
c	397	18.4	1.2	48	16	AAQ80730	Bombyx mori pBMHPC
c	398	18.4	1.2	48	19	AAV18209	Codon optimised si
c	399	18.4	1.2	48	22	AAL29496	Human SNP oligonuc
	400	18.4	1.2	48	22	AAS13891	Nodavirus RNA1 PCR
c	401	18.4	1.2	48	22	AAD13092	Oligo DEVA-2 for c
	402	18.4	1.2	49	15	AAQ69655	Human adenosine de
	403	18.4	1.2	49	18	AAT64117	Human adenosine de
	404	18.4	1.2	49	20	AAX17405	Test sequence from
	405	18.4	1.2	49	22	AAS13008	HIV-1 zinc binding
	406	18.4	1.2	49	23	ABA10640	Tail adaptor oligo
c	407	18.4	1.2	49	23	ABA10863	Tail adaptor oligo
	408	18.4	1.2	49	24	ABK82896	DNA binding molecu
	409	18.4	1.2	50	15	AAQ69731	Human ubiquitin-li
c	410	18.4	1.2	50	15	AAQ69376	Human erythropoiet
c	411	18.4	1.2	50	18	AAT76096	Human histidine de
	412	18.4	1.2	50	18	AAT64193	Human ubiquitin-li
c	413	18.4	1.2	50	18	AAT63838	Human erythropoiet
c	414	18.4	1.2	50	20	AAX53907	Histidine decarbox
	415	18.4	1.2	50	20	AAX17481	Test sequence from
c	416	18.4	1.2	50	20	AAX17126	Test sequence from
c	417	18.4	1.2	50	21	AAF19472	Human histidine de
c	418	18.4	1.2	50	21	AAA33350	Low adenosine anti
	419	18.4	1.2	50	22	AAL27894	Human SNP oligonuc
c	420	18.4	1.2	50	22	AAL28817	Human SNP oligonuc
c	421	18.4	1.2	50	22	AAL28896	Human SNP oligonuc
c	422	18.4	1.2	50	22	AAL29890	Human SNP oligonuc
	423	18.4	1.2	50	22	AAL30113	Human SNP oligonuc
	424	18.4	1.2	50	22	AAL30376	Human SNP oligonuc
c	425	18.4	1.2	50	22	AAL33675	Human SNP oligonuc
	426	18.4	1.2	50	22	AAL34180	Human SNP oligonuc
	427	18.4	1.2	50	22	AAL34303	Human SNP oligonuc
c	428	18.4	1.2	50	22	AAL34566	Human SNP oligonuc
	429	18.4	1.2	50	22	AAI78855	Human silent SNP c
c	430	18.4	1.2	50	23	ABL01021	Human SNP involvin
c	431	18.4	1.2	50	24	ABK82617	DNA binding molecu
	432	18.4	1.2	50	24	ABK82972	DNA binding molecu
c	433	18.4	1.2	50	24	ABK22703	Ets related gene (
c	434	18.4	1.2	50	24	ABK13347	Human transcriptio
	435	18.2	1.2	24	17	AAX15200	Central region seq
c	436	18.2	1.2	25	19	AAV59458	Hedgehog protein d
	437	18.2	1.2	31	22	AAH78572	Probe used to dete
	438	18.2	1.2	31	22	AAI31038	Human single nucle
	439	18.2	1.2	32	14	AAQ52007	B-cell mRNA ribozy
	440	18.2	1.2	34	19	AAV62416	Human Desert hedge
c	441	18.2	1.2	35	19	AAV36067	Oligonucleotide CB
	442	18.2	1.2	39	17	AAT35018	TIMP-1/fibronectin
	443	18.2	1.2	39	18	AAT86948	Primer used in MHC
	444	18.2	1.2	39	18	AAT87251	IL-4 2'NH2 RNA lig
	445	18.2	1.2	39	18	AAT87228	IL-4 2'NH2 RNA lig
c	446	18.2	1.2	40	14	AAQ50264	HIV env INS mutage
	447	18.2	1.2	40	21	AAZ95854	Polynucleotide seq
c	448	18.2	1.2	40	21	AAZ96142	Polynucleotide seq
c	449	18.2	1.2	40	22	AAF86312	PCR primer for amp
	450	18.2	1.2	41	15	AAQ62423	Vector pVAC1 const
	451	18.2	1.2	41	24	ABL56705	Probe #1 for human
	452	18.2	1.2	42	16	AAQ99066	(Gly4Ser)2 linker
	453	18.2	1.2	42	21	AAA12864	DNA encoding (Gly4
	454	18.2	1.2	42	21	AAA05766	Human growth hormo
	455	18.2	1.2	42	22	AAF74252	DNA analysis metho
c	456	18.2	1.2	43	24	ABL99298	Synthetic Renilla
	457	18.2	1.2	45	20	AAX82033	Mouse heavy chain
	458	18.2	1.2	45	20	AAX05564	Mouse heavy chain
	459	18.2	1.2	46	15	AAQ69434	Human heat shock p
	460	18.2	1.2	46	18	AAT63896	Human hsp70B gene
	461	18.2	1.2	46	20	AAX17184	Test sequence from
	462	18.2	1.2	46	24	ABK82675	DNA binding molecu
c	463	18.2	1.2	47	19	AAV44007	Human Mab #117/10C
c	464	18.2	1.2	47	21	AAZ67614	Human map-related
	465	18.2	1.2	47	21	AAZ69138	Human map-related
	466	18.2	1.2	47	23	ABA09881	Primer #62 from pr
	467	18.2	1.2	48	22	AAH97435	Human Chk1 ribozym
	468	18.2	1.2	48	22	AAF28330	eryAI gene KS1 seg
c	469	18.2	1.2	48	24	ABK15480	Urokinase plasmino
c	470	18.2	1.2	49	23	ABA10701	Tail adaptor oligo
	471	18.2	1.2	49	23	ABA10718	Tail adaptor oligo
	472	18.2	1.2	49	23	ABA10770	Tail adaptor oligo
	473	18.2	1.2	50	15	AAQ69581	Human non-histone
c	474	18.2	1.2	50	18	AAT85081	Human cytomegalovi
c	475	18.2	1.2	50	18	AAT73788	Multiplex short-PC
c	476	18.2	1.2	50	18	AAT73776	Multiplex short-PC
c	477	18.2	1.2	50	18	AAT73764	Multiplex short-PC
	478	18.2	1.2	50	18	AAT64043	Human non-histone
	479	18.2	1.2	50	20	AAX99200	M. intracellulare
	480	18.2	1.2	50	20	AAX99201	M. simium 16S rRNA
c	481	18.2	1.2	50	20	AAX80341	HCV NS4A-NS3 compl
c	482	18.2	1.2	50	20	AAX52094	Synthetic plasmid
	483	18.2	1.2	50	20	AAX17331	Test sequence from
	484	18.2	1.2	50	21	AAA77403	Human clone cg4492
c	485	18.2	1.2	50	22	AAL29583	Human SNP oligonuc
	486	18.2	1.2	50	22	AAL30020	Human SNP oligonuc
c	487	18.2	1.2	50	22	AAL31893	Human SNP oligonuc
c	488	18.2	1.2	50	22	AAL32412	Human SNP oligonuc
c	489	18.2	1.2	50	22	AAL34106	Human SNP oligonuc
	490	18.2	1.2	50	22	AAL34326	Human SNP oligonuc
c	491	18.2	1.2	50	22	AAL34565	Human SNP oligonuc
c	492	18.2	1.2	50	22	AAI78241	Human silent SNP c
c	493	18.2	1.2	50	22	AAH79788	Human DNA containi
	494	18.2	1.2	50	24	ABK82822	DNA binding molecu
c	495	18	1.1	18	22	AAH45474	PCR primer Shh-D s
	496	18	1.1	27	19	AAV94470	Canine IL-2 recept
	497	18	1.1	27	20	AAX55044	C/EBP-beta antisen
	498	18	1.1	27	21	AAF20613	Human C/EBP polynu
	499	18	1.1	27	21	AAA34491	Human adenosine re
	500	18	1.1	28	20	AAX55043	C/EBP-beta antisen
	501	18	1.1	28	21	AAF20612	Human C/EBP polynu
	502	18	1.1	28	21	AAA34490	Human adenosine re
	503	18	1.1	29	20	AAX55042	C/EBP-beta antisen
	504	18	1.1	29	21	AAF20611	Human C/EBP polynu
	505	18	1.1	29	21	AAA34489	Human adenosine re
	506	18	1.1	30	20	AAX55041	C/EBP-beta antisen
	507	18	1.1	30	21	AAF20610	Human C/EBP polynu
	508	18	1.1	30	21	AAA34488	Human adenosine re
	509	18	1.1	31	20	AAX55040	C/EBP-beta antisen
	510	18	1.1	31	21	AAF20609	Human C/EBP polynu
	511	18	1.1	31	21	AAA34487	Human adenosine re
	512	18	1.1	32	20	AAX55039	C/EBP-beta antisen
	513	18	1.1	32	21	AAF20608	Human C/EBP polynu
	514	18	1.1	32	21	AAA34486	Human adenosine re
	515	18	1.1	33	20	AAX55038	C/EBP-beta antisen
	516	18	1.1	33	21	AAF20607	Human C/EBP polynu
	517	18	1.1	33	21	AAA34485	Human adenosine re
c	518	18	1.1	33	24	AAS17985	Human zinc finger
	519	18	1.1	34	20	AAX55037	C/EBP-beta antisen
	520	18	1.1	34	21	AAF20606	Human C/EBP polynu

	521	18	1.1	34	21	AAA34484	Human adenosine re
	522	18	1.1	35	20	AAX89879	Monoclonal antibod
	523	18	1.1	35	20	AAX55036	C/EBP-beta antisen
	524	18	1.1	35	20	AAX55061	C/EBP-beta antisen
	525	18	1.1	35	20	AAV99232	PCR primer used to
	526	18	1.1	35	21	AAF20605	Human C/EBP polynu
	527	18	1.1	35	21	AAF20630	Human C/EBP polynu
	528	18	1.1	35	21	AAA72503	Degenerative oligo
	529	18	1.1	35	21	AAA34483	Human adenosine re
	530	18	1.1	35	21	AAA34508	Human adenosine re
c	531	18	1.1	36	15	AAQ73470	Porcine interleuki
c	532	18	1.1	36	19	AAV60887	Oligonucleotide 91
	533	18	1.1	36	20	AAX55035	C/EBP-beta antisen
	534	18	1.1	36	21	AAF20604	Human C/EBP polynu
	535	18	1.1	36	21	AAA34482	Human adenosine re
c	536	18	1.1	36	21	AAA35819	Permutein linker e
c	537	18	1.1	36	22	AAS11896	PCR primer PVX fla
	538	18	1.1	38	12	AAQ14201	Probe P1672 for Gi
	539	18	1.1	39	19	AAV21265	Tissue plasminogen
	540	18	1.1	40	22	AAF28274	Part of PsaA gene
	541	18	1.1	41	15	AAQ62421	Vector pVAC1 const
	542	18	1.1	41	19	AAV51143	Maize polymorphic
c	543	18	1.1	41	19	AAV47941	Maize polymorphic
	544	18	1.1	41	22	AAH75556	Human cathepsin 29
	545	18	1.1	42	14	AAQ34777	Multiple cloning s
	546	18	1.1	42	16	AAQ83950	Oligonucleotide cl
	547	18	1.1	42	17	AAT34411	Oligonucleotide 33
c	548	18	1.1	42	21	AAZ48717	PCR primer EGRE7 f
	549	18	1.1	42	24	ABN83751	Oligonucleotide us
	550	18	1.1	43	19	AAV43085	Amplification prim
	551	18	1.1	43	20	AAX01003	Error prone PCR pr
	552	18	1.1	43	24	AAD24760	Human immunodefici
	553	18	1.1	44	24	ABI82368	p53 mutation detec
	554	18	1.1	45	16	AAQ74158	Mouse heavy chain
	555	18	1.1	45	22	AAF67664	Xenopus insulator
	556	18	1.1	46	18	AAT69251	Flt-1 gene probe A
c	557	18	1.1	46	18	AAT87195	Interleukin-4 2'F
	558	18	1.1	46	20	AAX37822	Primer 7. Synthet
	559	18	1.1	47	20	AAX56656	Primer 29. Synthe
c	560	18	1.1	47	23	AAH88681	CNS disorder-relat
	561	18	1.1	48	15	AAQ69453	Human rearranged k
c	562	18	1.1	48	16	AAQ80731	Bombyx mori pBMHPC
	563	18	1.1	48	18	AAT63915	Human rearranged k
	564	18	1.1	48	20	AAX17203	Test sequence from
	565	18	1.1	48	21	AAC63541	Mutagenic primer 8
	566	18	1.1	48	21	AAC64499	Ecotin site direct
c	567	18	1.1	48	22	AAS13890	Nodavirus RNA1 PCR
	568	18	1.1	48	22	AAH22251	Anti-A33 antigen a
	569	18	1.1	48	22	AAH20116	Rabbit anti A33 an
	570	18	1.1	48	24	ABK82694	DNA binding molecu
	571	18	1.1	49	13	AAQ33591	Microsatellite seq
	572	18	1.1	49	23	ABA10665	Tail adaptor oligo
	573	18	1.1	49	23	ABA10688	Tail adaptor oligo
c	574	18	1.1	49	24	AAL43078	Regulatable, catal
c	575	18	1.1	50	15	AAQ69724	Human epidermal gr
	576	18	1.1	50	15	AAQ69624	Human bcl-2 proto-
	577	18	1.1	50	18	AAT76083	Human IgE receptor
c	578	18	1.1	50	18	AAT73762	Multiplex short-PC
	579	18	1.1	50	18	AAT65741	Repeat sequence fr
	580	18	1.1	50	18	AAT59919	Oligonucleotide pr
c	581	18	1.1	50	18	AAT64186	Human epidermal gr
	582	18	1.1	50	18	AAT64086	Human B-cell leuke
	583	18	1.1	50	20	AAX53891	Human IgE receptor
c	584	18	1.1	50	20	AAX17474	Test sequence from
	585	18	1.1	50	20	AAX17374	Test sequence from
	586	18	1.1	50	21	AAF19456	Human IgE receptor
	587	18	1.1	50	21	AAA59749	Oligomer I used to
	588	18	1.1	50	21	AAA33334	Low adenosine anti
c	589	18	1.1	50	22	AAL28011	Human SNP oligonuc
	590	18	1.1	50	22	AAL28644	Human SNP oligonuc
c	591	18	1.1	50	22	AAL28816	Human SNP oligonuc
c	592	18	1.1	50	22	AAL30158	Human SNP oligonuc
	593	18	1.1	50	22	AAL30651	Human SNP oligonuc
	594	18	1.1	50	22	AAL31846	Human SNP oligonuc
	595	18	1.1	50	22	AAL33721	Human SNP oligonuc
c	596	18	1.1	50	22	AAL34403	Human SNP oligonuc
c	597	18	1.1	50	22	AAI76329	Human silent SNP c
c	598	18	1.1	50	22	AAI76871	Human silent SNP c
	599	18	1.1	50	24	ABK82865	DNA binding molecu
c	600	18	1.1	50	24	ABK82965	DNA binding molecu
c	601	17.8	1.1	21	21	AAA95383	Rat Shh coding seq
c	602	17.8	1.1	21	21	AAZ49111	PCR primer for mou
c	603	17.8	1.1	29	23	ABL52929	Poliovirus vaccine
	604	17.8	1.1	30	18	AAT93621	GC-rich DNA probe.
c	605	17.8	1.1	30	23	ABL53308	Oligonucleotide li
	606	17.8	1.1	31	22	AAI29637	Human single nucle
	607	17.8	1.1	31	22	AAI30188	Human single nucle
	608	17.8	1.1	31	22	AAI30471	Human single nucle
c	609	17.8	1.1	32	18	AAT46190	Primer for 2',5'-o
c	610	17.8	1.1	32	20	AAV83776	Guamerin gene ampl
	611	17.8	1.1	33	19	AAV26185	BHV-1 gD gene PCR
	612	17.8	1.1	34	21	AAA12122	T. brucei trypanos
c	613	17.8	1.1	36	21	AAA35862	Permutein linker e
	614	17.8	1.1	38	23	ABL58030	Human Inverted CCA
	615	17.8	1.1	39	22	AAS45570	B cell lymphoma CJ
c	616	17.8	1.1	39	22	AAH74434	PCR primer used to
	617	17.8	1.1	39	22	AAH20260	CJ linker library
c	618	17.8	1.1	39	23	ABL58031	Human Inverted CCA
c	619	17.8	1.1	40	19	AAV15508	Primer for adeno-a
c	620	17.8	1.1	40	22	AAF28723	Template Nuc T16 f
c	621	17.8	1.1	41	19	AAV47702	Maize polymorphic
c	622	17.8	1.1	41	24	ABL41373	Human transcriptio
	623	17.8	1.1	41	24	ABA04239	Human phosphatase
	624	17.8	1.1	42	19	AAV23585	Primer for lucifer
	625	17.8	1.1	43	15	AAQ78841	HCMV Ab heavy chai
	626	17.8	1.1	44	17	AAT33026	Antibody H chain V
	627	17.8	1.1	44	20	AAX77430	PCR primer VH2aF5.
	628	17.8	1.1	44	21	AAC96958	PCR primer VH2aF5
c	629	17.8	1.1	45	15	AAQ55102	DNA encoding signa
c	630	17.8	1.1	45	15	AAQ69541	Human steroid 5-al
c	631	17.8	1.1	45	18	AAT64003	Human steroid 5-al
c	632	17.8	1.1	45	20	AAX17291	Test sequence from
c	633	17.8	1.1	45	21	AAA28616	Oligonucleotide MS
	634	17.8	1.1	45	22	AAC87939	B43 scFv cassette
	635	17.8	1.1	45	22	AAC87940	B43 scFv cassette
c	636	17.8	1.1	45	24	ABK82782	DNA binding molecu
c	637	17.8	1.1	46	12	AAQ14251	Proinsulin-tendami
c	638	17.8	1.1	46	12	AAQ14252	Proinsulin-tendami
	639	17.8	1.1	46	14	AAQ49093	P. multocida 16S r
	640	17.8	1.1	46	20	AAX22935	DE19736591 primer
c	641	17.8	1.1	46	22	AAF27354	PCR primer, SEQ ID
c	642	17.8	1.1	47	18	AAT73790	Multiplex short-PC
c	643	17.8	1.1	47	21	AAZ68163	Human map-related
	644	17.8	1.1	47	22	AAD20555	Human CITEDX (HCIT
c	645	17.8	1.1	48	12	AAQ12358	Europium-labelled
c	646	17.8	1.1	48	13	AAQ29924	Fruit fly cuticle
	647	17.8	1.1	48	16	AAQ81434	HBV target sequenc
	648	17.8	1.1	48	22	AAD13091	Oligo DEVA-1 for c
c	649	17.8	1.1	49	18	AAT73806	Multiplex short-PC
c	650	17.8	1.1	49	18	AAT73786	Multiplex short-PC
c	651	17.8	1.1	50	15	AAQ69787	Herpes simplex vir
c	652	17.8	1.1	50	18	AAT73801	Multiplex short-PC
c	653	17.8	1.1	50	18	AAT73804	Multiplex short-PC
c	654	17.8	1.1	50	18	AAT73781	Multiplex short-PC
c	655	17.8	1.1	50	18	AAT73774	Multiplex short-PC
c	656	17.8	1.1	50	18	AAT64249	HSV-2 18K (start s
c	657	17.8	1.1	50	20	AAX17537	Test sequence from
	658	17.8	1.1	50	22	AAL29277	Human SNP oligonuc
c	659	17.8	1.1	50	22	AAL29989	Human SNP oligonuc
c	660	17.8	1.1	50	22	AAL30007	Human SNP oligonuc
c	661	17.8	1.1	50	22	AAL32420	Human SNP oligonuc
	662	17.8	1.1	50	22	AAL34214	Human SNP oligonuc
c	663	17.8	1.1	50	22	AAL34375	Human SNP oligonuc
c	664	17.8	1.1	50	22	AAL34441	Human SNP oligonuc
c	665	17.8	1.1	50	22	AAL34573	Human SNP oligonuc
	666	17.8	1.1	50	22	AAD20877	Escherichia coli L

	667	17.8	1.1	50	22	AAI73843	Human silent SNP c
c	668	17.8	1.1	50	24	ABK83028	DNA binding molecu
c	669	17.8	1.1	50	24	AAS18936	Human CLASP-1 intr
	670	17.6	1.1	25	24	ABT03636	Human Hey-2 gene P
	671	17.6	1.1	27	18	AAT38815	Marmoset intracell
	672	17.6	1.1	28	21	AAZ43856	Human IgG4 heavy c
	673	17.6	1.1	28	22	AAH91324	Human inflammatory
	674	17.6	1.1	30	24	ABK27945	Lipolytic enzyme P
	675	17.6	1.1	31	18	AAT43522	Anti-lymphoma anti
c	676	17.6	1.1	31	20	AAX58868	Alfalfa aldose red
c	677	17.6	1.1	31	21	AAA79212	Human genomic DNA
	678	17.6	1.1	32	13	AAQ33551	Microsatellite seq
c	679	17.6	1.1	32	20	AAX76429	Sequencing reagent
c	680	17.6	1.1	32	21	AAA28513	Primer RIL 5' EcoR
	681	17.6	1.1	33	13	AAQ33565	Microsatellite seq
	682	17.6	1.1	34	16	AAQ78556	Gene-specific prim
	683	17.6	1.1	34	18	AAT80845	Gene specific prim
	684	17.6	1.1	35	20	AAV84061	Oligonucleotide of
c	685	17.6	1.1	36	14	AAQ52042	Breast cancer spec
c	686	17.6	1.1	36	18	AAT78495	RET proto-oncogene
c	687	17.6	1.1	36	22	AAS11861	Human collagen gen
	688	17.6	1.1	40	13	AAQ25025	Anti-sense oligonu
c	689	17.6	1.1	40	20	AAV83195	Primer for amplify
	690	17.6	1.1	40	21	AAZ95904	Polynucleotide seq
	691	17.6	1.1	40	21	AAZ96115	Polynucleotide seq
	692	17.6	1.1	41	15	AAQ69493	Human motilin gene
	693	17.6	1.1	41	18	AAT63955	Human motilin gene
c	694	17.6	1.1	41	19	AAV51140	Maize polymorphic
c	695	17.6	1.1	41	19	AAV51139	Maize polymorphic
	696	17.6	1.1	41	19	AAV47891	Maize polymorphic
	697	17.6	1.1	41	19	AAV44008	Human Mab #117/10C
c	698	17.6	1.1	41	20	AAZ23515	T cell receptor V
	699	17.6	1.1	41	20	AAX17243	Test sequence from
c	700	17.6	1.1	41	22	AAF84046	5' and 3' targetin
	701	17.6	1.1	41	24	ABK82734	DNA binding molecu
c	702	17.6	1.1	41	24	ABL40949	Slicing factor Prp
c	703	17.6	1.1	42	20	AAX23255	H. virescens JHE p
	704	17.6	1.1	42	21	AAA05763	Human growth hormo
c	705	17.6	1.1	42	21	AAA05767	Human growth hormo
	706	17.6	1.1	42	22	AAF67667	Xenopus insulator
	707	17.6	1.1	42	24	ABA93611	Human tau protein
	708	17.6	1.1	43	20	AAX78900	Non-replicative Va
c	709	17.6	1.1	43	22	AAC82204	Human retrovirus D
	710	17.6	1.1	44	14	AAQ50454	PCR Primer for amp
	711	17.6	1.1	44	14	AAQ50456	PCR primer for amp
c	712	17.6	1.1	44	15	AAQ64210	Degenerate probe f
	713	17.6	1.1	44	15	AAQ69313	Human sodium/potas
	714	17.6	1.1	44	18	AAT63775	Human Na/K ATPase
c	715	17.6	1.1	44	19	AAV43251	3' AAV-ITR primer
	716	17.6	1.1	44	20	AAX59211	Human antibody VH
	717	17.6	1.1	44	20	AAX17063	Test sequence from
	718	17.6	1.1	44	24	ABK82554	DNA binding molecu
	719	17.6	1.1	45	17	AAT42480	Primer for chimeri
c	720	17.6	1.1	45	20	AAX00855	Phage display libr
c	721	17.6	1.1	45	21	AAZ87269	DNA encoding FGFR-
	722	17.6	1.1	45	21	AAZ43463	Human scFV light a
c	723	17.6	1.1	45	21	AAZ43464	Human scFV light a
	724	17.6	1.1	45	21	AAZ43521	Human scFV light a
	725	17.6	1.1	45	24	ABN83130	Moloney leukaemia
	726	17.6	1.1	46	15	AAQ62448	Vector pVAC1 const
c	727	17.6	1.1	46	16	AAT02971	Gene delivery fusi
	728	17.6	1.1	46	17	AAT09697	C. elegans glutama
c	729	17.6	1.1	46	22	AAI74098	Human silent SNP c
c	730	17.6	1.1	47	18	AAT88017	Human interleukin
c	731	17.6	1.1	47	19	AAV45793	Vector pROCOS4/7 i
	732	17.6	1.1	47	20	AAZ01112	Probe for human PG
c	733	17.6	1.1	47	21	AAZ68369	Human map-related
	734	17.6	1.1	47	21	AAZ68664	Human map-related
c	735	17.6	1.1	47	23	AAH88358	CNS disorder-relat
	736	17.6	1.1	47	24	ABK86107	Human IGFBP3 site
	737	17.6	1.1	48	18	AAT64734	Phytase gene probe
	738	17.6	1.1	48	20	AAX00874	Nucleotide sequenc
	739	17.6	1.1	48	22	AAF28078	Nascent protein de
	740	17.6	1.1	48	24	ABK86064	Protein C mutant K
c	741	17.6	1.1	48	24	ABK86065	Protein C mutant K
c	742	17.6	1.1	49	18	AAT80517	Hepatoma AS-30D Ty
	743	17.6	1.1	49	18	AAT63974	Human amyloid A4 p
	744	17.6	1.1	49	20	AAX17262	Test sequence from
	745	17.6	1.1	49	23	ABA09759	Adaptor oligonucle
	746	17.6	1.1	49	23	ABA09868	Primer #49 from pr
	747	17.6	1.1	49	23	ABA10979	Tail adaptor oligo
	748	17.6	1.1	49	24	ABK82753	DNA binding molecu
c	749	17.6	1.1	50	12	AAQ15286	BMP-3 5' end probe
	750	17.6	1.1	50	15	AAQ69774	Herpes simplex vir
c	751	17.6	1.1	50	15	AAQ69841	Simian virus 40 T/
	752	17.6	1.1	50	18	AAT48644	Synthetic haipin o
	753	17.6	1.1	50	18	AAT61249	Human antibody kap
	754	17.6	1.1	50	18	AAT64236	HSV-1 b'g'a'TIF/VS
c	755	17.6	1.1	50	18	AAT64303	SV40 T/t early P2
	756	17.6	1.1	50	19	AAV49704	Human J chain targ
c	757	17.6	1.1	50	19	AAV10620	Primer for eryAI g
	758	17.6	1.1	50	20	AAX08857	Nucleotide used to
c	759	17.6	1.1	50	20	AAX17591	Test sequence from
	760	17.6	1.1	50	20	AAX17524	Test sequence from
c	761	17.6	1.1	50	21	AAA29070	3' PCR primer for
	762	17.6	1.1	50	21	AAZ99814	Nucleotide sequenc
c	763	17.6	1.1	50	22	AAL27949	Human SNP oligonuc
c	764	17.6	1.1	50	22	AAL28617	Human SNP oligonuc
	765	17.6	1.1	50	22	AAL28815	Human SNP oligonuc
c	766	17.6	1.1	50	22	AAL29050	Human SNP oligonuc
	767	17.6	1.1	50	22	AAL29363	Human SNP oligonuc
c	768	17.6	1.1	50	22	AAL30328	Human SNP oligonuc
c	769	17.6	1.1	50	22	AAL30920	Human SNP oligonuc
	770	17.6	1.1	50	22	AAL31600	Human SNP oligonuc
c	771	17.6	1.1	50	22	AAL32086	Human SNP oligonuc
	772	17.6	1.1	50	22	AAL33552	Human SNP oligonuc
	773	17.6	1.1	50	22	AAL33634	Human SNP oligonuc
c	774	17.6	1.1	50	22	AAL34014	Human SNP oligonuc
c	775	17.6	1.1	50	22	AAL34151	Human SNP oligonuc
	776	17.6	1.1	50	22	AAL34194	Human SNP oligonuc
c	777	17.6	1.1	50	22	AAL34195	Human SNP oligonuc
c	778	17.6	1.1	50	22	AAL34298	Human SNP oligonuc
	779	17.6	1.1	50	22	AAL34313	Human SNP oligonuc
c	780	17.6	1.1	50	22	AAL34327	Human SNP oligonuc
	781	17.6	1.1	50	22	AAL34411	Human SNP oligonuc
c	782	17.6	1.1	50	22	AAS43512	Corneodesmosin sin
	783	17.6	1.1	50	22	AAI75801	Human silent SNP c
c	784	17.6	1.1	50	22	AAH89754	Human coding sequ
	785	17.6	1.1	50	22	AAF30231	Oligonucleotide fo
	786	17.6	1.1	50	24	ABK97280	TM gene oligonucle
	787	17.6	1.1	50	24	ABK83015	DNA binding molecu
c	788	17.6	1.1	50	24	ABK83082	DNA binding molecu
	789	17.6	1.1	50	24	ABK47030	Adenovirus vectro
	790	17.4	1.1	26	20	AAZ23703	Human sonic hedgeh
	791	17.4	1.1	26	20	AAZ28439	Primer 344, for am
	792	17.4	1.1	26	24	ABK28815	HSV-2 capture sequ
c	793	17.4	1.1	27	14	AAQ40855	DNA sequence used
	794	17.4	1.1	27	14	AAQ40856	DNA sequence used
	795	17.4	1.1	30	18	AAT89034	Solid phase gene H
c	796	17.4	1.1	31	22	AAI29725	Human single nucle
c	797	17.4	1.1	31	22	AAI29731	Human single nucle
	798	17.4	1.1	31	22	AAI30723	Human single nucle
c	799	17.4	1.1	32	20	AAX21303	Human PKD protein
	800	17.4	1.1	34	18	AAT76246	Human IL6 receptor
	801	17.4	1.1	34	20	AAX54036	Human IL-6 recepto
	802	17.4	1.1	34	21	AAF19602	Human IL6 receptor
	803	17.4	1.1	34	21	AAA33479	Low adenosine anti
	804	17.4	1.1	34	21	AAA33480	Low adenosine anti
	805	17.4	1.1	34	22	AAH45806	Human RNA helicase
	806	17.4	1.1	35	22	AAI67126	B. licheniformis a
	807	17.4	1.1	35	22	AAH42693	PCR primer used to
	808	17.4	1.1	35	22	AAF62585	Oligonucleotide 17
	809	17.4	1.1	36	16	AAT57645	RSV N hammerhead r
c	810	17.4	1.1	36	19	AAV37232	Primer for bovine
c	811	17.4	1.1	36	20	AAX55009	C/EBP-beta antisen
c	812	17.4	1.1	36	21	AAF20578	Human C/EBP polynu

c	813	17.4	1.1	36	21	AAA34456	Human adenosine re
c	814	17.4	1.1	37	20	AAX55008	C/EBP-beta antisen
c	815	17.4	1.1	37	21	AAF20577	Human C/EBP polynu
c	816	17.4	1.1	37	21	AAA34455	Human adenosine re
c	817	17.4	1.1	37	24	AAS19086	Human chorionic go
	818	17.4	1.1	38	17	AAT15807	Humanised LL2 MAb
	819	17.4	1.1	38	18	AAT88132	Primer for variabl
c	820	17.4	1.1	38	20	AAX55007	C/EBP-beta antisen
c	821	17.4	1.1	38	21	AAF20576	Human C/EBP polynu
c	822	17.4	1.1	38	21	AAA34454	Human adenosine re
	823	17.4	1.1	38	24	ABL31969	FokI/FspI containi
	824	17.4	1.1	38	24	ABL31971	FokI/FspI containi
c	825	17.4	1.1	39	20	AAX55006	C/EBP-beta antisen
c	826	17.4	1.1	39	21	AAF20575	Human C/EBP polynu
c	827	17.4	1.1	39	21	AAA34453	Human adenosine re
c	828	17.4	1.1	39	21	AAZ60139	PCR primer C2 used
c	829	17.4	1.1	39	24	ABL91539	Chlamydia pneumoni
c	830	17.4	1.1	40	20	AAX55005	C/EBP-beta antisen
c	831	17.4	1.1	40	21	AAF20574	Human C/EBP polynu
c	832	17.4	1.1	40	21	AAA09439	M. alpina delta-6
c	833	17.4	1.1	40	21	AAA34452	Human adenosine re
c	834	17.4	1.1	41	20	AAX55004	C/EBP-beta antisen
	835	17.4	1.1	41	20	AAX22756	Human ESRP1 DNA PC
c	836	17.4	1.1	41	21	AAF20573	Human C/EBP polynu
c	837	17.4	1.1	41	21	AAA34451	Human adenosine re
c	838	17.4	1.1	41	24	ABL53417	tRNA guanine glyco
	839	17.4	1.1	42	20	AAX57794	Reverse primer for
c	840	17.4	1.1	42	20	AAX55003	C/EBP-beta antisen
c	841	17.4	1.1	42	21	AAF20572	Human C/EBP polynu
c	842	17.4	1.1	42	21	AAA34450	Human adenosine re
	843	17.4	1.1	42	22	AAC86365	Linker used to mak
	844	17.4	1.1	43	9	AAN82099	Oligonucleotide pr
	845	17.4	1.1	43	10	AAN94347	Probe for 2,5-dike
c	846	17.4	1.1	43	20	AAX55002	C/EBP-beta antisen
c	847	17.4	1.1	43	21	AAF20571	Human C/EBP polynu
c	848	17.4	1.1	43	21	AAA34449	Human adenosine re
	849	17.4	1.1	44	15	AAQ69402	Human GST pi gene
	850	17.4	1.1	44	18	AAT63864	Human GST pi gene
	851	17.4	1.1	44	20	AAX59209	Human antibody VH
c	852	17.4	1.1	44	20	AAX55001	C/EBP-beta antisen
	853	17.4	1.1	44	20	AAX17152	Test sequence from
c	854	17.4	1.1	44	21	AAF20570	Human C/EBP polynu
c	855	17.4	1.1	44	21	AAA34448	Human adenosine re
c	856	17.4	1.1	44	22	AAH19349	Human platelet-der
	857	17.4	1.1	44	24	ABK82643	DNA binding molecu
	858	17.4	1.1	45	12	AAQ12281	Probe to minisatel
	859	17.4	1.1	45	12	AAQ12282	Probe to minisatel
c	860	17.4	1.1	45	15	AAQ69449	Human insulin-like
c	861	17.4	1.1	45	16	AAQ80726	Bombyx mori sex sp
c	862	17.4	1.1	45	18	AAT63911	Human IGF binding
c	863	17.4	1.1	45	19	AAV18215	Codon optimised si
c	864	17.4	1.1	45	20	AAX55000	C/EBP-beta antisen
c	865	17.4	1.1	45	20	AAX54966	C/EBP-beta antisen
c	866	17.4	1.1	45	20	AAX17199	Test sequence from
c	867	17.4	1.1	45	21	AAF20535	Human C/EBP polynu
c	868	17.4	1.1	45	21	AAF20569	Human C/EBP polynu
c	869	17.4	1.1	45	21	AAA34413	Human adenosine re
c	870	17.4	1.1	45	21	AAA34447	Human adenosine re
c	871	17.4	1.1	45	21	AAA05786	Streptavidin displ
c	872	17.4	1.1	45	24	ABK82690	DNA binding molecu
c	873	17.4	1.1	45	24	AAD35831	Rat galanin recept
	874	17.4	1.1	46	16	AAT08345	The Nf-kB ELAM 2 b
c	875	17.4	1.1	46	20	AAX54965	C/EBP-beta antisen
c	876	17.4	1.1	46	21	AAF20534	Human C/EBP polynu
c	877	17.4	1.1	46	21	AAA34412	Human adenosine re
c	878	17.4	1.1	46	22	AAF27030	Human Desert hedge
	879	17.4	1.1	47	15	AAQ69263	Human beta-actin g
	880	17.4	1.1	47	18	AAT63725	Human beta-actin g
	881	17.4	1.1	47	20	AAX56657	Primer 30. Synthe
	882	17.4	1.1	47	20	AAX56659	Primer 32. Synthe
	883	17.4	1.1	47	20	AAX17013	Test sequence from
	884	17.4	1.1	47	21	AAZ65789	Human map-related
	885	17.4	1.1	47	21	AAZ67439	Human map-related
c	886	17.4	1.1	47	21	AAZ68973	Human map-related
	887	17.4	1.1	47	22	AAF30323	Human gamma 1 cons
	888	17.4	1.1	47	24	ABK82504	DNA binding molecu
	889	17.4	1.1	47	24	ABA99916	Chicken tenascin t
	890	17.4	1.1	48	16	AAT02970	Gene delivery fusi
	891	17.4	1.1	48	22	AAD06901	Human oligo 8 to c
	892	17.4	1.1	48	22	AAI64404	PCR primer #11. U
c	893	17.4	1.1	49	22	AAS13008	HIV-1 zinc binding
	894	17.4	1.1	50	12	AAQ15286	BMP-3 5' end probe
	895	17.4	1.1	50	17	AAX35091	Oligonucleotide wh
	896	17.4	1.1	50	17	AAT41693	Oligonucleotide co
	897	17.4	1.1	50	17	AAT37108	Oligonucleotide ha
	898	17.4	1.1	50	21	AAA77273	Human clone cg4398
	899	17.4	1.1	50	21	AAC11348	Human secreted pro
	900	17.4	1.1	50	21	AAC11563	Human secreted pro
	901	17.4	1.1	50	22	AAL28563	Human SNP oligonuc
	902	17.4	1.1	50	22	AAL28816	Human SNP oligonuc
	903	17.4	1.1	50	22	AAL29078	Human SNP oligonuc
c	904	17.4	1.1	50	22	AAL29236	Human SNP oligonuc
c	905	17.4	1.1	50	22	AAL29415	Human SNP oligonuc
	906	17.4	1.1	50	22	AAL29449	Human SNP oligonuc
	907	17.4	1.1	50	22	AAL29799	Human SNP oligonuc
	908	17.4	1.1	50	22	AAL29803	Human SNP oligonuc
	909	17.4	1.1	50	22	AAL30007	Human SNP oligonuc
	910	17.4	1.1	50	22	AAL31229	Human SNP oligonuc
c	911	17.4	1.1	50	22	AAL31322	Human SNP oligonuc
	912	17.4	1.1	50	22	AAL34058	Human SNP oligonuc
	913	17.4	1.1	50	22	AAL34106	Human SNP oligonuc
	914	17.4	1.1	50	22	AAL34299	Human SNP oligonuc
c	915	17.4	1.1	50	22	AAL34331	Human SNP oligonuc
c	916	17.4	1.1	50	22	AAL34547	Human SNP oligonuc
c	917	17.4	1.1	50	22	AAL34585	Human SNP oligonuc
	918	17.4	1.1	50	22	AAI73276	Human silent SNP c
	919	17.4	1.1	50	22	AAI76535	Human silent SNP c
	920	17.4	1.1	50	22	AAI76857	Human silent SNP c
	921	17.4	1.1	50	22	AAI76859	Human silent SNP c
c	922	17.4	1.1	50	22	AAI77727	Human silent SNP c
	923	17.4	1.1	50	22	AAI78355	Human silent SNP c
c	924	17.4	1.1	50	22	AAH89775	Human coding sequ
c	925	17.4	1.1	50	22	AAH90532	Human clone cg4397
c	926	17.4	1.1	50	22	AAD11597	Non-target oligo N
	927	17.4	1.1	50	23	AAS15626	Human beta 2 micro
	928	17.4	1.1	50	23	AAS15627	Human HLA-A2 PCR p
	929	17.4	1.1	50	24	ABQ75849	PCR primer for amp
c	930	17.2	1.1	24	20	AAX01774	Human cystic fibro
	931	17.2	1.1	24	21	AAA64229	RACE PCR primer JA
c	932	17.2	1.1	24	22	AAF74610	Cystic fibrosis tr
c	933	17.2	1.1	25	20	AAX55142	C/EBP-beta antisen
c	934	17.2	1.1	25	21	AAF20711	Human C/EBP polynu
c	935	17.2	1.1	25	21	AAA34589	Human adenosine re
c	936	17.2	1.1	26	9	AAN82048	Probe O-CCR-26 for
	937	17.2	1.1	30	13	AAQ20870	Immunostimulatory
c	938	17.2	1.1	30	13	AAQ20873	Immunostimulatory
	939	17.2	1.1	30	13	AAQ24607	Primer BDG-122. S
c	940	17.2	1.1	30	20	AAZ08169	HTRT sequence-spec
c	941	17.2	1.1	30	21	AAA05778	Streptavidin displ
	942	17.2	1.1	30	21	AAZ39175	Human BMP-4 5' ups
	943	17.2	1.1	30	22	AAF99891	Immunostimulatory
c	944	17.2	1.1	30	22	AAF99891	Immunostimulatory
c	945	17.2	1.1	30	23	AAS13774	Simple sequence re
	946	17.2	1.1	30	23	AAS13789	Simple sequence re
c	947	17.2	1.1	30	23	AAS13789	Simple sequence re
	948	17.2	1.1	30	24	AAL42352	Novel sand pear mi
	949	17.2	1.1	31	13	AAQ33543	Microsatellite seq
	950	17.2	1.1	31	22	AAI30043	Human single nucle
c	951	17.2	1.1	31	22	AAI31038	Human single nucle
c	952	17.2	1.1	32	18	AAT76227	Human IL5 antisens
c	953	17.2	1.1	32	20	AAX54023	Human IL-5 antisen
c	954	17.2	1.1	32	21	AAF19589	Human IL5 polynucl
c	955	17.2	1.1	32	21	AAA33467	Low adenosine anti
c	956	17.2	1.1	32	21	AAZ48716	PCR primer EGRP6 f
	957	17.2	1.1	33	13	AAQ29687	Oligonucleotide pr
	958	17.2	1.1	33	21	AAZ43426	Hybrid ScFV-3-19 p

c 959	17.2	1.1	35	19	AAT99119	Synthetic PCR prim
960	17.2	1.1	35	21	AAZ58685	Anti-CD4 antibody
961	17.2	1.1	35	21	AAZ44227	Murine CD4/CD34 re
962	17.2	1.1	36	20	AAV72065	806.077 scFv antib
963	17.2	1.1	36	21	AAA35919	Permutein linker e
964	17.2	1.1	37	17	AAT38703	Primer for DNA enc
965	17.2	1.1	37	21	AAZ28955	PCR primer mu-ATG2
966	17.2	1.1	38	12	AAQ14197	Probe P1446 for Gi
c 967	17.2	1.1	38	12	AAQ14795	fdTetBSN vector ol
c 968	17.2	1.1	38	20	AAX59828	Probe used to dete
969	17.2	1.1	38	20	AAX59829	Probe used to dete
970	17.2	1.1	39	14	AAQ51915	c-myc mRNA ribozym
c 971	17.2	1.1	39	22	AAD18455	T. vulgaris (Tvu)
c 972	17.2	1.1	39	22	AAH47403	Mutant Tvu DNA pol
c 973	17.2	1.1	40	12	AAQ11990	Probe Sq918 to ena
c 974	17.2	1.1	40	13	AAQ25018	Sense oligonucleot
c 975	17.2	1.1	40	18	AAT47465	Foldback triplex f
c 976	17.2	1.1	40	18	AAT47475	Foldback triplex f
977	17.2	1.1	40	19	AAV47799	Maize polymorphic
978	17.2	1.1	40	21	AAA12119	T. brucei trypanos
c 979	17.2	1.1	40	21	AAZ95915	Polynucleotide seq
980	17.2	1.1	40	21	AAZ95991	Polynucleotide seq
981	17.2	1.1	40	21	AAZ57137	Quadruplex DNA SEQ
982	17.2	1.1	41	15	AAQ58775	Human glucagon rec
983	17.2	1.1	41	15	AAQ62422	Vector pVAC1 const
984	17.2	1.1	41	15	AAQ62424	Vector pVAC1 const
985	17.2	1.1	41	15	AAQ62442	Vector pVAC1 const
c 986	17.2	1.1	41	19	AAV50937	Maize polymorphic
987	17.2	1.1	41	19	AAV50609	Brassica sp. polym
c 988	17.2	1.1	41	19	AAV47888	Maize polymorphic
989	17.2	1.1	41	24	ABL41573	Probe #1 relating
c 990	17.2	1.1	41	24	ABA99840	Human TGF-beta 110
c 991	17.2	1.1	41	24	AAS16440	Human hydrogenase
c 992	17.2	1.1	42	16	AAQ86675	NF-AT transcriptio
c 993	17.2	1.1	42	17	AAT27160	Human Machado-Jose
994	17.2	1.1	42	17	AAT14495	HuMN14 Fab/F(ab')2
995	17.2	1.1	42	18	AAT94056	Oligo used in cons
996	17.2	1.1	42	18	AAT80027	Primer #3 for tumo
c 997	17.2	1.1	42	20	AAZ24679	Oligonucleotide fo
998	17.2	1.1	42	20	AAX36430	PCR primer for Hum
c 999	17.2	1.1	42	21	AAA29261	Human nuclear fact
c1000	17.2	1.1	42	22	AAH73847	Thermal amplificat

ALIGNMENTS

RESULT 1
AAD09047/c
ID AAD09047 standard; DNA; 50 BP.
XX
AC AAD09047;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human oligonucleotide HOG-403 used to construct pKS285.
XX
KW Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant;
KW cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
KW Huntington's chorea; amylotropic lateral sclerosis; multiple sclerosis;
KW nervous system aging; neurodegenerative disease; immunological disease;
KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
KW extracellular signalling protein; HOG-403; ss.
XX
OS Homo sapiens.
XX
PN WO200134654-A1.
XX
PD 17-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US30405.
XX
PR 05-NOV-1999; 99US-0164025.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Strauch K;
XX
DR WPI; 2001-329075/34.
XX
PT Novel isolated hedgehog fusion polypeptide useful for treating
PT neurological conditions such as Alzheimer's disease, Parkinson's
PT disease, Huntington's chorea, amylotropic lateral sclerosis, and
PT multiple sclerosis -
XX
PS Example 1; Page 60; 178pp; English.
XX
CC The present invention relates to hedgehog fusion proteins. Hedgehog
CC proteins are a family of extracellular signalling proteins that regulate
CC various aspects of embryonic development both in vertebrates and in
CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
CC treatment of any condition or disease state for which a hedgehog or
CC patched protein constituent is efficacious and in the diagnosis of
CC constituents or conditions of disease states in biological system or
CC specimens and for diagnostic purposes in non-physiological systems.
CC Hedgehog fusion protein is useful for treating neurological conditions
CC due to injury, aging of nervous system, including Alzheimer's disease,
CC chronic neurodegenerative diseases of the nervous system, including
CC Parkinson's disease, Huntington's chorea, amylotropic lateral sclerosis
CC and chronic immunological diseases of nervous system including multiple
CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
CC tumours and to specifically target medical therapies against cancers and
CC tumours which express the receptor for the protein. The present sequence
CC is human oligonucleotide HOG-403 used to construct pKS285, pKS288,
CC pKS309, pKS310, pKS287 pKS300 and pKS289 plasmids which are used in the
CC invention.
XX
SQ Sequence 50 BP; 11 A; 11 C; 15 G; 13 T; 0 other;

Query Match 3.2%; Score 50; DB 22; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 CCTTTAGCCTACAAGCAGTTTATCCCCAATGTGGCCGAGAAGACCCTAGG 321
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 50 CCTTTAGCCTACAAGCAGTTTATCCCCAATGTGGCCGAGAAGACCCTAGG 1

RESULT 2
AAD09078/c
ID AAD09078 standard; DNA; 50 BP.
XX
AC AAD09078;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human oligonucleotide HOG-803 used to construct pMMC22.
XX
KW Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant;
KW cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
KW Huntington's chorea; amylotropic lateral sclerosis; multiple sclerosis;
KW nervous system aging; neurodegenerative disease; immunological disease;
KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
KW extracellular signalling protein; HOG-803; ss.
XX
OS Homo sapiens.
XX
PN WO200134654-A1.
XX
PD 17-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US30405.
XX
PR 05-NOV-1999; 99US-0164025.
XX
PA (BIOJ) BIOGEN INC.

XX
PI Strauch K;
XX
DR WPI; 2001-329075/34.
XX
PT Novel isolated hedgehog fusion polypeptide useful for treating
PT neurological conditions such as Alzheimer's disease, Parkinson's
PT disease, Huntington's chorea, amylotropic lateral sclerosis, and
PT multiple sclerosis -
XX
PS Example 1; Page 62; 178pp; English.
XX
CC The present invention relates to hedgehog fusion proteins. Hedgehog
CC proteins are a family of extracellular signalling proteins that regulate
CC various aspects of embryonic development both in vertebrates and in
CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
CC treatment of any condition or disease state for which a hedgehog or
CC patched protein constituent is efficacious and in the diagnosis of
CC constituents or conditions of disease states in biological system or
CC specimens and for diagnostic purposes in non-physiological systems.
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CC due to injury, aging of nervous system, including Alzheimer's disease,
CC chronic neurodegenerative diseases of the nervous system, including
CC Parkinson's disease, Huntington's chorea, amylotropic lateral sclerosis
CC and chronic immunological diseases of nervous system including multiple
CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
CC tumours and to specifically target medical therapies against cancers and
CC tumours which express the receptor for the protein. The present sequence
CC is human oligonucleotide HOG-803 used to construct pMMC22 plasmid which
CC is used in the invention.
XX
SQ Sequence 50 BP; 6 A; 17 C; 13 G; 14 T; 0 other;

Query Match 3.1%; Score 48.4; DB 22; Length 50;
Best Local Similarity 98.0%; Pred. No. 14;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 228 CGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACCCCTTTA 277
||||||||||||||||||||| ||||||||||||||||||||||||||||
Db 50 CGGGCAGGGGGTTCGGGAAGAAGAGGCACCCCAAAAAGCTGACCCCTTTA 1

RESULT 3
AAD09079/c
ID AAD09079 standard; DNA; 50 BP.
XX
AC AAD09079;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human oligonucleotide HOG-804 used to construct pMMC23.
XX
KW Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant;
KW cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
KW Huntington's chorea; amylotropic lateral sclerosis; multiple sclerosis;
KW nervous system aging; neurodegenerative disease; immunological disease;
KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
KW extracellular signalling protein; HOG-804; ss.
XX
OS Homo sapiens.
XX
PN WO200134654-A1.
XX
PD 17-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US30405.
XX
PR 05-NOV-1999; 99US-0164025.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Strauch K;
XX
DR WPI; 2001-329075/34.
XX
PT Novel isolated hedgehog fusion polypeptide useful for treating
PT neurological conditions such as Alzheimer's disease, Parkinson's
PT disease, Huntington's chorea, amylotropic lateral sclerosis, and
PT multiple sclerosis -
XX
PS Example 1; Page 62; 178pp; English.
XX
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CC proteins are a family of extracellular signalling proteins that regulate
CC various aspects of embryonic development both in vertebrates and in
CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
CC treatment of any condition or disease state for which a hedgehog or
CC patched protein constituent is efficacious and in the diagnosis of
CC constituents or conditions of disease states in biological system or
CC specimens and for diagnostic purposes in non-physiological systems.
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CC due to injury, aging of nervous system, including Alzheimer's disease,
CC chronic neurodegenerative diseases of the nervous system, including
CC Parkinson's disease, Huntington's chorea, amylotropic lateral sclerosis
CC and chronic immunological diseases of nervous system including multiple
CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
CC tumours and to specifically target medical therapies against cancers and
CC tumours which express the receptor for the protein. The present sequence
CC is human oligonucleotide HOG-804 used to construct pMMC23 plasmid which
CC is used in the invention.
XX
SQ Sequence 50 BP; 6 A; 19 C; 13 G; 12 T; 0 other;

Query Match 3.1%; Score 48.4; DB 22; Length 50;
Best Local Similarity 98.0%; Pred. No. 14;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 228 CGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACCCCTTTA 277
||||||||||||||||||| ||||||||||||||||||||||||||||
Db 50 CGGGCAGGGGGTTCGGGAGGAGGAGGCACCCCAAAAAGCTGACCCCTTTA 1

RESULT 4
AAD09081/c
ID AAD09081 standard; DNA; 50 BP.
XX
AC AAD09081;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human oligonucleotide HOG-807 used to construct pMMC26.
XX
KW Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant;
KW cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
KW Huntington's chorea; amylotropic lateral sclerosis; multiple sclerosis;
KW nervous system aging; neurodegenerative disease; immunological disease;
KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
KW extracellular signalling protein; HOG-807; ss.
XX
OS Homo sapiens.
XX
PN WO200134654-A1.
XX
PD 17-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US30405.
XX
PR 05-NOV-1999; 99US-0164025.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Strauch K;
XX
DR WPI; 2001-329075/34.
XX
PT Novel isolated hedgehog fusion polypeptide useful for treating

PT neurological conditions such as Alzheimer's disease, Parkinson's
PT disease, Huntington's chorea, amylotropic lateral sclerosis, and
PT multiple sclerosis -
XX
PS Example 1; Page 62; 178pp; English.
XX
CC The present invention relates to hedgehog fusion proteins. Hedgehog
CC proteins are a family of extracellular signalling proteins that regulate
CC various aspects of embryonic development both in vertebrates and in
CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
CC treatment of any condition or disease state for which a hedgehog or
CC patched protein constituent is efficacious and in the diagnosis of
CC constituents or conditions of disease states in biological system or
CC specimens and for diagnostic purposes in non-physiological systems.
CC Hedgehog fusion protein is useful for treating neurological conditions
CC due to injury, aging of nervous system, including Alzheimer's disease,
CC chronic neurodegenerative diseases of the nervous system, including
CC Parkinson's disease, Huntington's chorea, amylotropic lateral sclerosis
CC and chronic immunological diseases of nervous system including multiple
CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
CC tumours and to specifically target medical therapies against cancers and
CC tumours which express the receptor for the protein. The present sequence
CC is human oligonucleotide HOG-807 used to construct pMMC26 plasmid which
CC is used in the invention.
XX
SQ Sequence 50 BP; 6 A; 19 C; 15 G; 10 T; 0 other;

Query Match 2.9%; Score 45.2; DB 22; Length 50;
Best Local Similarity 94.0%; Pred. No. 47;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 228 CGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACCCCTTTA 277
||||||||||||||||||||||||||||||| | ||||||||||||||
Db 50 CGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCCAGCAGCTGACCCCTTTA 1

RESULT 5
AAD09073
ID AAD09073 standard; DNA; 47 BP.
XX
AC AAD09073;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human oligonucleotide HOG-789 used to construct pMMC22.
XX
KW Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant;
KW cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
KW Huntington's chorea; amylotropic lateral sclerosis; multiple sclerosis;
KW nervous system aging; neurodegenerative disease; immunological disease;
KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
KW extracellular signalling protein; HOG-789; ss.
XX
OS Homo sapiens.
XX
PN WO200134654-A1.
XX
PD 17-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US30405.
XX
PR 05-NOV-1999; 99US-0164025.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Strauch K;
XX
DR WPI; 2001-329075/34.
XX
PT Novel isolated hedgehog fusion polypeptide useful for treating
PT neurological conditions such as Alzheimer's disease, Parkinson's
PT disease, Huntington's chorea, amylotropic lateral sclerosis, and
PT multiple sclerosis -
XX
PS Example 1; Page 61; 178pp; English.
XX
CC The present invention relates to hedgehog fusion proteins. Hedgehog
CC proteins are a family of extracellular signalling proteins that regulate
CC various aspects of embryonic development both in vertebrates and in
CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
CC treatment of any condition or disease state for which a hedgehog or
CC patched protein constituent is efficacious and in the diagnosis of
CC constituents or conditions of disease states in biological system or
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CC due to injury, aging of nervous system, including Alzheimer's disease,
CC chronic neurodegenerative diseases of the nervous system, including
CC Parkinson's disease, Huntington's chorea, amylotropic lateral sclerosis
CC and chronic immunological diseases of nervous system including multiple
CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
CC tumours and to specifically target medical therapies against cancers and
CC tumours which express the receptor for the protein. The present sequence
CC is human oligonucleotide HOG-789 used to construct pMMC22 plasmid which
CC is used in the invention.
XX
SQ Sequence 47 BP; 13 A; 13 C; 18 G; 3 T; 0 other;

Query Match 2.8%; Score 43.8; DB 22; Length 47;
Best Local Similarity 95.7%; Pred. No. 81;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 225 GACCGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACC 271
| ||||||||||||||||||||||| |||||||||||||||||||||
Db 1 GCCCGGGCAGGGGGTTCGGGAAGAAGAGGCACCCCAAAAAGCTGACC 47

RESULT 6
AAD09074
ID AAD09074 standard; DNA; 47 BP.
XX
AC AAD09074;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human oligonucleotide HOG-791 used to construct pMMC23.
XX
KW Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant;
KW cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
KW Huntington's chorea; amylotropic lateral sclerosis; multiple sclerosis;
KW nervous system aging; neurodegenerative disease; immunological disease;
KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
KW extracellular signalling protein; HOG-791; ss.
XX
OS Homo sapiens.
XX
PN WO200134654-A1.
XX
PD 17-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US30405.
XX
PR 05-NOV-1999; 99US-0164025.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Strauch K;
XX
DR WPI; 2001-329075/34.
XX
PT Novel isolated hedgehog fusion polypeptide useful for treating
PT neurological conditions such as Alzheimer's disease, Parkinson's
PT disease, Huntington's chorea, amylotropic lateral sclerosis, and
PT multiple sclerosis -
XX
PS Example 1; Page 61-62; 178pp; English.
XX

CC The present invention relates to hedgehog fusion proteins. Hedgehog
CC proteins are a family of extracellular signalling proteins that regulate
CC various aspects of embryonic development both in vertebrates and in
CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
CC treatment of any condition or disease state for which a hedgehog or
CC patched protein constituent is efficacious and in the diagnosis of
CC constituents or conditions of disease states in biological system or
CC specimens and for diagnostic purposes in non-physiological systems.
CC Hedgehog fusion protein is useful for treating neurological conditions
CC due to injury, aging of nervous system, including Alzheimer's disease,
CC chronic neurodegenerative diseases of the nervous system, including
CC Parkinson's disease, Huntington's chorea, amylotropic lateral sclerosis
CC and chronic immunological diseases of nervous system including multiple
CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
CC tumours and to specifically target medical therapies against cancers and
CC tumours which express the receptor for the protein. The present sequence
CC is human oligonucleotide HOG-791 used to construct pMMC23 plasmid which
CC is used in the invention.
XX
SQ Sequence 47 BP; 11 A; 13 C; 20 G; 3 T; 0 other;

Query Match 2.8%; Score 43.8; DB 22; Length 47;
Best Local Similarity 95.7%; Pred. No. 81;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 225 GACCGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACC 271
| |||||||||||||||||| |||||||||||||||||||||||||
Db 1 GCCCGGGCAGGGGGTTCGGGAGGAGGAGGCACCCCAAAAAGCTGACC 47

RESULT 7
AAD09077
ID AAD09077 standard; DNA; 45 BP.
XX
AC AAD09077;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human oligonucleotide HOG-799 used to construct pMMC22.
XX
KW Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant;
KW cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
KW Huntington's chorea; amylotropic lateral sclerosis; multiple sclerosis;
KW nervous system aging; neurodegenerative disease; immunological disease;
KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
KW extracellular signalling protein; HOG-799; ss.
XX
OS Homo sapiens.
XX
PN WO200134654-A1.
XX
PD 17-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US30405.
XX
PR 05-NOV-1999; 99US-0164025.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Strauch K;
XX
DR WPI; 2001-329075/34.
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PT neurological conditions such as Alzheimer's disease, Parkinson's
PT disease, Huntington's chorea, amylotropic lateral sclerosis, and
PT multiple sclerosis -
XX
PS Example 1; Page 62; 178pp; English.
XX
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CC proteins are a family of extracellular signalling proteins that regulate
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CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
CC treatment of any condition or disease state for which a hedgehog or
CC patched protein constituent is efficacious and in the diagnosis of
CC constituents or conditions of disease states in biological system or
CC specimens and for diagnostic purposes in non-physiological systems.
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CC due to injury, aging of nervous system, including Alzheimer's disease,
CC chronic neurodegenerative diseases of the nervous system, including
CC Parkinson's disease, Huntington's chorea, amylotropic lateral sclerosis
CC and chronic immunological diseases of nervous system including multiple
CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
CC tumours and to specifically target medical therapies against cancers and
CC tumours which express the receptor for the protein. The present sequence
CC is human oligonucleotide HOG-799 used to construct pMMC22, pMMC23, pMMC25
CC and pMMC26 plasmids which are used in the invention.
XX
SQ Sequence 45 BP; 12 A; 14 C; 10 G; 9 T; 0 other;

Query Match 2.8%; Score 43.4; DB 22; Length 45;
Best Local Similarity 97.8%; Pred. No. 95;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 272 CCTTTAGCCTACAAGCAGTTTATCCCCAATGTGGCCGAGAAGACC 316
||||||||||||||||||||||||||||| ||||||||||||||
Db 1 CCTTTAGCCTACAAGCAGTTTATCCCCAAGGTGGCCGAGAAGACC 45

RESULT 8
AAF27031/c
ID AAF27031 standard; DNA; 48 BP.
XX
AC AAF27031;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:35.
XX
KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
KW bioavailibility; formulation; neurological disorder;
KW inflammatory disorder; autoimmune disorder; cancer;
KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW malignant glioma; medulloblastoma; neuroectodermal tumour;
KW mutagenic primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200073337-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14741.
XX
PR 01-JUN-1999; 99US-0137011.
PR 13-AUG-1999; 99US-0149016.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Pepinsky RB, Taylor F, Garber E;
XX
DR WPI; 2001-049927/06.
XX
PT Modified hedgehog protein, useful in the treatment of Parkinson's
PT disease and Huntington's chorea, comprises a polymer containing a
PT polyalkylene glycol group linked to any residue other than the
PT N-terminal and lysine residues -
XX
PS Example 6; Page 77; 157pp; English.
XX
CC The invention relates to novel polymer conjugates of hedgehog proteins
CC which have increased bioavailability. The hedgehog proteins are
CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene

CC glycol group, with the proviso that the polymer is not conjugated to the
CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
CC a hedgehog fusion protein. The invention also relates to methods of
CC defining and mapping functionally important regions of a protein by
CC modifying accessible amino acid side chains, and determining the effect
CC the position and/or type of modification have on the activity of the
CC protein. The hedgehog polymer conjugates may be used in the management of
CC various medical conditions including various neurological disorders,
CC inflammatory and autoimmune diseases, and cancers. In particular, they
CC may be used to prevent preventing or ameliorate neurodegenerative
CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
CC disease); age-associated neurological disease; neurological injury and
CC trauma; immunological diseases of the nervous system (e.g., multiple
CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
CC neuroectodermal tumours. The modifications made to the hedgehog protein
CC may result in increased half-life, altered tissue distribution (such as
CC an improved ability to stay in the vasculature for longer periods of
CC time), increased stability in solution, protection from proteolytic
CC degradation, or reduced immunogenicity. In particular, the ability to
CC remain in the vasculature for prolonged periods may allow a hedgehog
CC protein of the invention to cross the blood-brain barrier, and an
CC increased thermal stability would be an advantage when formulating the
CC hedgehog protein in powder form. The present sequence represents a
CC human Sonic hedgehog mutagenic primer used in an exemplification of the
CC invention.
XX
SQ Sequence 48 BP; 10 A; 13 C; 15 G; 10 T; 0 other;

Query Match 2.7%; Score 43.2; DB 22; Length 48;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy    278 GCCTACAAGCAGTTTATCCCCAATGTGGCCGAGAAGACCCTAGGCGCC 325
          |||||||||||||||||||||  |||||| ||||||||||||||||||
Db     48 GCCTACAAGCAGTTTATCCCCTGTGTGGCTGAGAAGACCCTAGGCGCC 1
```

RESULT 9
AAF27034/c
ID AAF27034 standard; DNA; 48 BP.
XX
AC AAF27034;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:38.
XX
KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
KW bioavailibility; formulation; neurological disorder;
KW inflammatory disorder; autoimmune disorder; cancer;
KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW malignant glioma; medulloblastoma; neuroectodermal tumour;
KW mutagenic primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200073337-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14741.
XX
PR 01-JUN-1999; 99US-0137011.
PR 13-AUG-1999; 99US-0149016.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Pepinsky RB, Taylor F, Garber E;
XX
DR WPI; 2001-049927/06.
XX
PT Modified hedgehog protein, useful in the treatment of Parkinson's
PT disease and Huntington's chorea, comprises a polymer containing a
PT polyalkylene glycol group linked to any residue other than the
PT N-terminal and lysine residues -
XX
PS Example 6; Page 77; 157pp; English.
XX
CC The invention relates to novel polymer conjugates of hedgehog proteins
CC which have increased bioavailability. The hedgehog proteins are
CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
CC glycol group, with the proviso that the polymer is not conjugated to the
CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
CC a hedgehog fusion protein. The invention also relates to methods of
CC defining and mapping functionally important regions of a protein by
CC modifying accessible amino acid side chains, and determining the effect
CC the position and/or type of modification have on the activity of the
CC protein. The hedgehog polymer conjugates may be used in the management of
CC various medical conditions including various neurological disorders,
CC inflammatory and autoimmune diseases, and cancers. In particular, they
CC may be used to prevent preventing or ameliorate neurodegenerative
CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
CC disease); age-associated neurological disease; neurological injury and
CC trauma; immunological diseases of the nervous system (e.g., multiple
CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
CC neuroectodermal tumours. The modifications made to the hedgehog protein
CC may result in increased half-life, altered tissue distribution (such as
CC an improved ability to stay in the vasculature for longer periods of
CC time), increased stability in solution, protection from proteolytic
CC degradation, or reduced immunogenicity. In particular, the ability to
CC remain in the vasculature for prolonged periods may allow a hedgehog
CC protein of the invention to cross the blood-brain barrier, and an
CC increased thermal stability would be an advantage when formulating the
CC hedgehog protein in powder form. The present sequence represents a
CC human Sonic hedgehog mutagenic primer used in an exemplification of the
CC invention.
XX
SQ Sequence 48 BP; 10 A; 15 C; 7 G; 16 T; 0 other;

Query Match 2.7%; Score 43.2; DB 22; Length 48;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy    398 GACATCATATTTAAGGATGAAGAAAACACCGGAGCGGACAGGCTGATG 445
          |||||||||||||||||||||||||   ||||||||||||||||||||
Db     48 GACATCATATTTAAGGATGAAGAATGTACCGGAGCGGACAGGCTGATG 1
```

RESULT 10
AAD09080/c
ID AAD09080 standard; DNA; 50 BP.
XX
AC AAD09080;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human oligonucleotide HOG-806 used to construct pMMC25.
XX
KW Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant;
KW cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
KW Huntington's chorea; amylotropic lateral sclerosis; multiple sclerosis;
KW nervous system aging; neurodegenerative disease; immunological disease;
KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
KW extracellular signalling protein; HOG-806; ss.
XX
OS Homo sapiens.
XX
PN WO200134654-A1.
XX
PD 17-MAY-2001.

XX
PF 02-NOV-2000; 2000WO-US30405.
XX
PR 05-NOV-1999; 99US-0164025.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Strauch K;
XX
DR WPI; 2001-329075/34.
XX
PT Novel isolated hedgehog fusion polypeptide useful for treating
PT neurological conditions such as Alzheimer's disease, Parkinson's
PT disease, Huntington's chorea, amylotropic lateral sclerosis, and
PT multiple sclerosis -
XX
PS Example 1; Page 62; 178pp; English.
XX
CC The present invention relates to hedgehog fusion proteins. Hedgehog
CC proteins are a family of extracellular signalling proteins that regulate
CC various aspects of embryonic development both in vertebrates and in
CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
CC treatment of any condition or disease state for which a hedgehog or
CC patched protein constituent is efficacious and in the diagnosis of
CC constituents or conditions of disease states in biological system or
CC specimens and for diagnostic purposes in non-physiological systems.
CC Hedgehog fusion protein is useful for treating neurological conditions
CC due to injury, aging of nervous system, including Alzheimer's disease,
CC chronic neurodegenerative diseases of the nervous system, including
CC Parkinson's disease, Huntington's chorea, amylotropic lateral sclerosis
CC and chronic immunological diseases of nervous system including multiple
CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
CC tumours and to specifically target medical therapies against cancers and
CC tumours which express the receptor for the protein. The present sequence
CC is human oligonucleotide HOG-806 used to construct pMMC25 plasmid which
CC is used in the invention.
XX
SQ Sequence 50 BP; 6 A; 16 C; 16 G; 12 T; 0 other;

Query Match 2.7%; Score 42; DB 22; Length 50;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 228 CGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACCCCTTTA 277
||||||||||||||||| || | ||||||||||||||||||||||||
Db 50 CGGGCAGGGGGTTCGGGCAGCAGCAGCACCCCAAAAAGCTGACCCCTTTA 1

RESULT 11
AAD09082/c
ID AAD09082 standard; DNA; 43 BP.
XX
AC AAD09082;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human oligonucleotide HOG-808 used to construct pMMC22.
XX
KW Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant;
KW cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
KW Huntington's chorea; amylotropic lateral sclerosis; multiple sclerosis;
KW nervous system aging; neurodegenerative disease; immunological disease;
KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
KW extracellular signalling protein; HOG-808; ss.
XX
OS Homo sapiens.
XX
PN WO200134654-A1.
XX
PD 17-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US30405.
XX
PR 05-NOV-1999; 99US-0164025.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Strauch K;
XX
DR WPI; 2001-329075/34.
XX
PT Novel isolated hedgehog fusion polypeptide useful for treating
PT neurological conditions such as Alzheimer's disease, Parkinson's
PT disease, Huntington's chorea, amylotropic lateral sclerosis, and
PT multiple sclerosis -
XX
PS Example 1; Page 62; 178pp; English.
XX
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CC proteins are a family of extracellular signalling proteins that regulate
CC various aspects of embryonic development both in vertebrates and in
CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
CC treatment of any condition or disease state for which a hedgehog or
CC patched protein constituent is efficacious and in the diagnosis of
CC constituents or conditions of disease states in biological system or
CC specimens and for diagnostic purposes in non-physiological systems.
CC Hedgehog fusion protein is useful for treating neurological conditions
CC due to injury, aging of nervous system, including Alzheimer's disease,
CC chronic neurodegenerative diseases of the nervous system, including
CC Parkinson's disease, Huntington's chorea, amylotropic lateral sclerosis
CC and chronic immunological diseases of nervous system including multiple
CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
CC tumours and to specifically target medical therapies against cancers and
CC tumours which express the receptor for the protein. The present sequence
CC is human oligonucleotide HOG-808 used to construct pMMC22, pMMC23, pMMC25
CC and pMMC26 plasmids which are used in the invention.
XX
SQ Sequence 43 BP; 8 A; 10 C; 14 G; 11 T; 0 other;

Query Match 2.6%; Score 41.4; DB 22; Length 43;
Best Local Similarity 97.7%; Pred. No. 2.1e+02;
Matches 42; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 278 GCCTACAAGCAGTTTATCCCCAATGTGGCCGAGAAGACCCTAG 320
|||||||||||| |||||||||||||||||||||||||||||
Db 43 GCCTACAAGCAGTTTCTCCCCAATGTGGCCGAGAAGACCCTAG 1

RESULT 12
AAD09076
ID AAD09076 standard; DNA; 47 BP.
XX
AC AAD09076;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human oligonucleotide HOG-797 used to construct pMMC26.
XX
KW Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant;
KW cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
KW Huntington's chorea; amylotropic lateral sclerosis; multiple sclerosis;
KW nervous system aging; neurodegenerative disease; immunological disease;
KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
KW extracellular signalling protein; HOG-797; ss.
XX
OS Homo sapiens.
XX
PN WO200134654-A1.
XX
PD 17-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US30405.
XX
PR 05-NOV-1999; 99US-0164025.
XX
PA (BIOJ) BIOGEN INC.

```
XX
PI   Strauch K;
XX
DR   WPI; 2001-329075/34.
XX
PT   Novel isolated hedgehog fusion polypeptide useful for treating
PT   neurological conditions such as Alzheimer's disease, Parkinson's
PT   disease, Huntington's chorea, amylotropic lateral sclerosis, and
PT   multiple sclerosis -
XX
PS   Example 1; Page 62; 178pp; English.
XX
CC   The present invention relates to hedgehog fusion proteins. Hedgehog
CC   proteins are a family of extracellular signalling proteins that regulate
CC   various aspects of embryonic development both in vertebrates and in
CC   invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
CC   treatment of any condition or disease state for which a hedgehog or
CC   patched protein constituent is efficacious and in the diagnosis of
CC   constituents or conditions of disease states in biological system or
CC   specimens and for diagnostic purposes in non-physiological systems.
CC   Hedgehog fusion protein is useful for treating neurological conditions
CC   due to injury, aging of nervous system, including Alzheimer's disease,
CC   chronic neurodegenerative diseases of the nervous system, including
CC   Parkinson's disease, Huntington's chorea, amylotropic lateral sclerosis
CC   and chronic immunological diseases of nervous system including multiple
CC   sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
CC   tumours and to specifically target medical therapies against cancers and
CC   tumours which express the receptor for the protein. The present sequence
CC   is human oligonucleotide HOG-797 used to construct pMMC23 plasmid which
CC   is used in the invention.
XX
SQ   Sequence 47 BP; 9 A; 15 C; 20 G; 3 T; 0 other;

  Query Match             2.6%;  Score 40.6;  DB 22;  Length 47;
  Best Local Similarity   91.5%;  Pred. No. 2.8e+02;
  Matches   43;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     225 GACCGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACC 271
           | |||||||||||||||||||||||||||||||| |  ||||||||
Db       1 GCCCGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCCAGCAGCTGACC 47


RESULT 13
AAD09075
ID   AAD09075 standard; DNA; 47 BP.
XX
AC   AAD09075;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human oligonucleotide HOG-795 used to construct pMMC25 plasmid.
XX
KW   Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant;
KW   cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
KW   Huntington's chorea; amylotropic lateral sclerosis; multiple sclerosis;
KW   nervous system aging; neurodegenerative disease; immunological disease;
KW   malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
KW   extracellular signalling protein; HOG-795; ss.
XX
OS   Homo sapiens.
XX
PN   WO200134654-A1.
XX
PD   17-MAY-2001.
XX
PF   02-NOV-2000; 2000WO-US30405.
XX
PR   05-NOV-1999;   99US-0164025.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Strauch K;
XX
DR   WPI; 2001-329075/34.
XX
PT   Novel isolated hedgehog fusion polypeptide useful for treating
PT   neurological conditions such as Alzheimer's disease, Parkinson's
PT   disease, Huntington's chorea, amylotropic lateral sclerosis, and
PT   multiple sclerosis -
XX
PS   Example 1; Page 62; 178pp; English.
XX
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CC   proteins are a family of extracellular signalling proteins that regulate
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CC   invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
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CC   patched protein constituent is efficacious and in the diagnosis of
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CC   Parkinson's disease, Huntington's chorea, amylotropic lateral sclerosis
CC   and chronic immunological diseases of nervous system including multiple
CC   sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
CC   tumours and to specifically target medical therapies against cancers and
CC   tumours which express the receptor for the protein. The present sequence
CC   is human oligonucleotide HOG-795 used to construct pMMC25 plasmid which
CC   is used in the invention.
XX
SQ   Sequence 47 BP; 11 A; 16 C; 17 G; 3 T; 0 other;

  Query Match             2.4%;  Score 37.4;  DB 22;  Length 47;
  Best Local Similarity   87.2%;  Pred. No. 9.6e+02;
  Matches   41;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     225 GACCGGGCAGGGGGTTCGGGAAGAGGAGGCACCCCAAAAAGCTGACC 271
           | |||||||||||||||||| ||  |  ||||||||||||||||||
Db       1 GCCCGGGCAGGGGGTTCGGGCAGCAGCAGCACCCCAAAAAGCTGACC 47


RESULT 14
AAF27032/c
ID   AAF27032 standard; DNA; 42 BP.
XX
AC   AAF27032;
XX
DT   30-MAR-2001  (first entry)
XX
DE   Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:36.
XX
KW   Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
KW   bioavailibility; formulation; neurological disorder;
KW   inflammatory disorder; autoimmune disorder; cancer;
KW   neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW   Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW   malignant glioma; medulloblastoma; neuroectodermal tumour;
KW   mutagenic primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200073337-A1.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US14741.
XX
PR   01-JUN-1999;   99US-0137011.
PR   13-AUG-1999;   99US-0149016.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Pepinsky RB,  Taylor F,  Garber E;
XX
```

DR WPI; 2001-049927/06.
XX
PT Modified hedgehog protein, useful in the treatment of Parkinson's
PT disease and Huntington's chorea, comprises a polymer containing a
PT polyalkylene glycol group linked to any residue other than the
PT N-terminal and lysine residues -
XX
PS Example 6; Page 77; 157pp; English.
XX
CC The invention relates to novel polymer conjugates of hedgehog proteins
CC which have increased bioavailability. The hedgehog proteins are
CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
CC glycol group, with the proviso that the polymer is not conjugated to the
CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
CC a hedgehog fusion protein. The invention also relates to methods of
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CC modifying accessible amino acid side chains, and determining the effect
CC the position and/or type of modification have on the activity of the
CC protein. The hedgehog polymer conjugates may be used in the management of
CC various medical conditions including various neurological disorders,
CC inflammatory and autoimmune diseases, and cancers. In particular, they
CC may be used to prevent preventing or ameliorate neurodegenerative
CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
CC disease); age-associated neurological disease; neurological injury and
CC trauma; immunological diseases of the nervous system (e.g., multiple
CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
CC neuroectodermal tumours. The modifications made to the hedgehog protein
CC may result in increased half-life, altered tissue distribution (such as
CC an improved ability to stay in the vasculature for longer periods of
CC time), increased stability in solution, protection from proteolytic
CC degradation, or reduced immunogenicity. In particular, the ability to
CC remain in the vasculature for prolonged periods may allow a hedgehog
CC protein of the invention to cross the blood-brain barrier, and an
CC increased thermal stability would be an advantage when formulating the
CC hedgehog protein in powder form. The present sequence represents a
CC human Sonic hedgehog mutagenic primer used in an exemplification of the
CC invention.
XX
SQ Sequence 42 BP; 8 A; 13 C; 9 G; 12 T; 0 other;

Query Match 2.4%; Score 37.2; DB 22; Length 42;
Best Local Similarity 92.9%; Pred. No. 1e+03;
Matches 39; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 338 GAAGGGAAGATCTCCAGAAACTCCGAGCGATTTAAGGAACTC 379
||||||||||||||||| |||||||||||||||||||
Db 42 GAAGGGAAGATCTCCAGGTGCTCCGAGCGATTTAAGGAACTC 1

RESULT 15
AAF27036/c
ID AAF27036 standard; DNA; 42 BP.
XX
AC AAF27036;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:40.
XX
KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
KW bioavailibility; formulation; neurological disorder;
KW inflammatory disorder; autoimmune disorder; cancer;
KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW malignant glioma; medulloblastoma; neuroectodermal tumour;
KW mutagenic primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200073337-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14741.
XX
PR 01-JUN-1999; 99US-0137011.
PR 13-AUG-1999; 99US-0149016.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Pepinsky RB, Taylor F, Garber E;
XX
DR WPI; 2001-049927/06.
XX
PT Modified hedgehog protein, useful in the treatment of Parkinson's
PT disease and Huntington's chorea, comprises a polymer containing a
PT polyalkylene glycol group linked to any residue other than the
PT N-terminal and lysine residues -
XX
PS Example 6; Page 77; 157pp; English.
XX
CC The invention relates to novel polymer conjugates of hedgehog proteins
CC which have increased bioavailability. The hedgehog proteins are
CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
CC glycol group, with the proviso that the polymer is not conjugated to the
CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
CC a hedgehog fusion protein. The invention also relates to methods of
CC defining and mapping functionally important regions of a protein by
CC modifying accessible amino acid side chains, and determining the effect
CC the position and/or type of modification have on the activity of the
CC protein. The hedgehog polymer conjugates may be used in the management of
CC various medical conditions including various neurological disorders,
CC inflammatory and autoimmune diseases, and cancers. In particular, they
CC may be used to prevent preventing or ameliorate neurodegenerative
CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
CC disease); age-associated neurological disease; neurological injury and
CC trauma; immunological diseases of the nervous system (e.g., multiple
CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
CC neuroectodermal tumours. The modifications made to the hedgehog protein
CC may result in increased half-life, altered tissue distribution (such as
CC an improved ability to stay in the vasculature for longer periods of
CC time), increased stability in solution, protection from proteolytic
CC degradation, or reduced immunogenicity. In particular, the ability to
CC remain in the vasculature for prolonged periods may allow a hedgehog
CC protein of the invention to cross the blood-brain barrier, and an
CC increased thermal stability would be an advantage when formulating the
CC hedgehog protein in powder form. The present sequence represents a
CC human Sonic hedgehog mutagenic primer used in an exemplification of the
CC invention.
XX
SQ Sequence 42 BP; 11 A; 14 C; 9 G; 8 T; 0 other;

Query Match 2.4%; Score 37.2; DB 22; Length 42;
Best Local Similarity 92.9%; Pred. No. 1e+03;
Matches 39; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 474 CTTTGGCCATCTCGGTGATGAACCAGTGGCCAGGAGTGAAAC 515
||||||||||||||||||| |||||||||||||||||||
Db 42 CTTTGGCCATCTCGGTGATGTGTCAGTGGCCAGGAGTGAAAC 1

RESULT 16
AAF27039/c
ID AAF27039 standard; DNA; 38 BP.
XX
AC AAF27039;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:43.
XX

KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
KW bioavailibility; formulation; neurological disorder;
KW inflammatory disorder; autoimmune disorder; cancer;
KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW malignant glioma; medulloblastoma; neuroectodermal tumour;
KW mutagenic primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200073337-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14741.
XX
PR 01-JUN-1999; 99US-0137011.
PR 13-AUG-1999; 99US-0149016.
XX
PA (BIOJ) BIOGEN INC.
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PI Pepinsky RB, Taylor F, Garber E;
XX
DR WPI; 2001-049927/06.
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PT disease and Huntington's chorea, comprises a polymer containing a
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CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
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CC may result in increased half-life, altered tissue distribution (such as
CC an improved ability to stay in the vasculature for longer periods of
CC time), increased stability in solution, protection from proteolytic
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CC remain in the vasculature for prolonged periods may allow a hedgehog
CC protein of the invention to cross the blood-brain barrier, and an
CC increased thermal stability would be an advantage when formulating the
CC hedgehog protein in powder form. The present sequence represents a
CC human Sonic hedgehog mutagenic primer used in an exemplification of the
CC invention.
XX
SQ Sequence 38 BP; 8 A; 11 C; 9 G; 10 T; 0 other;

Query Match 2.3%; Score 36.4; DB 22; Length 38;
Best Local Similarity 97.4%; Pred. No. 1.4e+03;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 662 GACTGGGTGTACTACGAGTCCAAGGCACATATCCACTG 699
||||||||||||||||||| ||||||||||||||||||
Db 38 GACTGGGTGTACTACGAGTGCAAGGCACATATCCACTG 1

RESULT 17
AAF27025/c
ID AAF27025 standard; DNA; 49 BP.
XX
AC AAF27025;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:29.
XX
KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
KW bioavailibility; formulation; neurological disorder;
KW inflammatory disorder; autoimmune disorder; cancer;
KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW malignant glioma; medulloblastoma; neuroectodermal tumour;
KW mutagenic primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200073337-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14741.
XX
PR 01-JUN-1999; 99US-0137011.
PR 13-AUG-1999; 99US-0149016.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Pepinsky RB, Taylor F, Garber E;
XX
DR WPI; 2001-049927/06.
XX
PT Modified hedgehog protein, useful in the treatment of Parkinson's
PT disease and Huntington's chorea, comprises a polymer containing a
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PT N-terminal and lysine residues -
XX
PS Example 2; Page 67; 157pp; English.
XX
CC The invention relates to novel polymer conjugates of hedgehog proteins
CC which have increased bioavailability. The hedgehog proteins are
CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
CC glycol group, with the proviso that the polymer is not conjugated to the
CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
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CC degradation, or reduced immunogenicity. In particular, the ability to
CC remain in the vasculature for prolonged periods may allow a hedgehog
CC protein of the invention to cross the blood-brain barrier, and an
CC increased thermal stability would be an advantage when formulating the
CC hedgehog protein in powder form. The present sequence represents a

CC human Sonic hedgehog mutagenic primer used in an exemplification of the
CC invention.
XX
SQ Sequence 49 BP; 8 A; 18 C; 9 G; 14 T; 0 other;

Query Match 2.3%; Score 36; DB 22; Length 49;
Best Local Similarity 88.6%; Pred. No. 1.7e+03;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 703 GGTGAAAGCAGAGAACTCGGTGGCGGCCAAATCGGGAGGCTGCT 746
||||||||||||||||||||| || ||||||||||||| |
Db 49 GGTGAAAGCAGAGAACTCGGTGTGCGCAAAATCGGGAGGCTGAT 6

RESULT 18
AAF27038/c
ID AAF27038 standard; DNA; 39 BP.
XX
AC AAF27038;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:42.
XX
KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
KW bioavailibility; formulation; neurological disorder;
KW inflammatory disorder; autoimmune disorder; cancer;
KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW malignant glioma; medulloblastoma; neuroectodermal tumour;
KW mutagenic primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200073337-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14741.
XX
PR 01-JUN-1999; 99US-0137011.
PR 13-AUG-1999; 99US-0149016.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Pepinsky RB, Taylor F, Garber E;
XX
DR WPI; 2001-049927/06.
XX
PT Modified hedgehog protein, useful in the treatment of Parkinson's
PT disease and Huntington's chorea, comprises a polymer containing a
PT polyalkylene glycol group linked to any residue other than the
PT N-terminal and lysine residues -
XX
PS Example 6; Page 77; 157pp; English.
XX
CC The invention relates to novel polymer conjugates of hedgehog proteins
CC which have increased bioavailability. The hedgehog proteins are
CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
CC glycol group, with the proviso that the polymer is not conjugated to the
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CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
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CC remain in the vasculature for prolonged periods may allow a hedgehog
CC protein of the invention to cross the blood-brain barrier, and an
CC increased thermal stability would be an advantage when formulating the
CC hedgehog protein in powder form. The present sequence represents a
CC human Sonic hedgehog mutagenic primer used in an exemplification of the
CC invention.
XX
SQ Sequence 39 BP; 7 A; 12 C; 13 G; 7 T; 0 other;

Query Match 2.3%; Score 35.8; DB 22; Length 39;
Best Local Similarity 94.9%; Pred. No. 1.8e+03;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 597 CCACGTCTGACCGCGACCGCAGCAAGTACGGCATGCTGG 635
|||||||||||||||| ||| ||||||||||||||||||
Db 39 CCACGTCTGACCGCGATCGCTGCAAGTACGGCATGCTGG 1

RESULT 19
AAF27035/c
ID AAF27035 standard; DNA; 42 BP.
XX
AC AAF27035;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:39.
XX
KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
KW bioavailibility; formulation; neurological disorder;
KW inflammatory disorder; autoimmune disorder; cancer;
KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW malignant glioma; medulloblastoma; neuroectodermal tumour;
KW mutagenic primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200073337-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14741.
XX
PR 01-JUN-1999; 99US-0137011.
PR 13-AUG-1999; 99US-0149016.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Pepinsky RB, Taylor F, Garber E;
XX
DR WPI; 2001-049927/06.
XX
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PT disease and Huntington's chorea, comprises a polymer containing a
PT polyalkylene glycol group linked to any residue other than the
PT N-terminal and lysine residues -
XX
PS Example 6; Page 77; 157pp; English.
XX
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CC increased thermal stability would be an advantage when formulating the
CC hedgehog protein in powder form. The present sequence represents a
CC human Sonic hedgehog mutagenic primer used in an exemplification of the
CC invention.
XX
SQ Sequence 42 BP; 11 A; 11 C; 10 G; 10 T; 0 other;

Query Match 2.3%; Score 35.6; DB 22; Length 42;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 38; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 445 GACTCAGAGGTGTAAGGACAAGTTGAACGCTTTGGCCATCTC 486
||||||||||||||||||| || ||||||||||||||||
Db 42 GACTCAGAGGTGTAAGGACTGCTTAAACGCTTTGGCCATCTC 1

RESULT 20
AAF27037/c
ID AAF27037 standard; DNA; 37 BP.
XX
AC AAF27037;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:41.
XX
KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
KW bioavailibility; formulation; neurological disorder;
KW inflammatory disorder; autoimmune disorder; cancer;
KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW malignant glioma; medulloblastoma; neuroectodermal tumour;
KW mutagenic primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200073337-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14741.
XX
PR 01-JUN-1999; 99US-0137011.
PR 13-AUG-1999; 99US-0149016.
XX
PA (BIOJ) BIOGEN INC.
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PI Pepinsky RB, Taylor F, Garber E;
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DR WPI; 2001-049927/06.
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CC human Sonic hedgehog mutagenic primer used in an exemplification of the
CC invention.
XX
SQ Sequence 37 BP; 6 A; 10 C; 12 G; 9 T; 0 other;

Query Match 2.1%; Score 33.8; DB 22; Length 37;
Best Local Similarity 94.6%; Pred. No. 3.9e+03;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 538 CGAAGATGGCCACCACTCAGAGGAGTCTCTGCACTAC 574
|||||||||||||||| ||||||||||||||||||
Db 37 CGAAGATGGCCACCACTGCGAGGAGTCTCTGCACTAC 1

RESULT 21
AAF27041/c
ID AAF27041 standard; DNA; 35 BP.
XX
AC AAF27041;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:45.
XX
KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
KW bioavailibility; formulation; neurological disorder;
KW inflammatory disorder; autoimmune disorder; cancer;
KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW malignant glioma; medulloblastoma; neuroectodermal tumour;
KW mutagenic primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200073337-A1.
XX

PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14741.
XX
PR 01-JUN-1999; 99US-0137011.
PR 13-AUG-1999; 99US-0149016.
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PA (BIOJ) BIOGEN INC.
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PI Pepinsky RB, Taylor F, Garber E;
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DR WPI; 2001-049927/06.
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CC invention.
XX
SQ Sequence 35 BP; 8 A; 15 C; 9 G; 3 T; 0 other;

Query Match 2.1%; Score 33.4; DB 22; Length 35;
Best Local Similarity 97.1%; Pred. No. 4.6e+03;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 639 GCCTGGCGGTGGAGGCCGGCTTCGACTGGGTGTAC 673
|||||||||||||||||| ||||||||||||||||||
Db 35 GCCTGGCGGTGGAGGCCTGCTTCGACTGGGTGTAC 1

RESULT 22
AAF27040/c
ID AAF27040 standard; DNA; 37 BP.
XX
AC AAF27040;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:44.
XX
KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
KW bioavailibility; formulation; neurological disorder;
KW inflammatory disorder; autoimmune disorder; cancer;
KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW malignant glioma; medulloblastoma; neuroectodermal tumour;
KW mutagenic primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200073337-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14741.
XX
PR 01-JUN-1999; 99US-0137011.
PR 13-AUG-1999; 99US-0149016.
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PA (BIOJ) BIOGEN INC.
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PI Pepinsky RB, Taylor F, Garber E;
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DR WPI; 2001-049927/06.
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CC hedgehog protein in powder form. The present sequence represents a
CC human Sonic hedgehog mutagenic primer used in an exemplification of the
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XX
SQ Sequence 37 BP; 7 A; 8 C; 13 G; 9 T; 0 other;

Query Match 2.0%; Score 32.2; DB 22; Length 37;
Best Local Similarity 91.9%; Pred. No. 7.2e+03;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 538 CGAAGATGGCCACCACTCAGAGGAGTCTCTGCACTAC 574
|||||||||||||||||| ||||||||||||||
Db 37 CGAAGATGGCCACCACTCATGCGAGTCTCTGCACTAC 1

```
RESULT 23
ABT03768/c
ID   ABT03768 standard; DNA; 27 BP.
XX
AC   ABT03768;
XX
DT   13-SEP-2002  (first entry)
XX
DE   Human SHH gene PCR primer SEQ ID NO: 289.
XX
KW   Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
KW   transcription factor; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200240716-A2.
XX
PD   23-MAY-2002.
XX
PF   13-NOV-2001; 2001WO-US43461.
XX
PR   16-NOV-2000; 2000US-249508P.
XX
PA   (CEMI-) CEMINES LLC.
XX
PI   Palm K;
XX
DR   WPI; 2002-537346/57.
XX
PT   Determining the presence of neoplastic molecular markers, by
PT   identifying the presence of markers in host test sample using array of
PT   neoplastic molecular marker specific reagents and analyzing the array
PT   of the reagents  -
XX
PS   Example 1; Page 19; 41pp; English.
XX
CC   The present invention relates to a method for determining the presence of
CC   neoplastic molecular markers in a host, involving the use of neoplastic
CC   molecular marker specific reagents to detect such markers and analysing
CC   the array of reagents, allowing the identification of the neoplastic
CC   disease present. This can be used to determine the best treatment for
CC   cancers, in particular neural cell, lung and prostate tumours. The
CC   present sequence is a PCR primer useful for detecting the coding
CC   sequences of markers of the invention.
XX
SQ   Sequence 27 BP; 3 A; 11 C; 9 G; 4 T; 0 other;

  Query Match             1.7%;  Score 27;  DB 24;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+04;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    755 TCGGCCACGGTGCACCTGGAGCAGGGC 781
          |||||||||||||||||||||||||||
Db     27 TCGGCCACGGTGCACCTGGAGCAGGGC 1


RESULT 24
AAQ33571
ID   AAQ33571 standard; DNA; 46 BP.
XX
AC   AAQ33571;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Microsatellite sequence from clone AGLA259.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US00340.
XX
PR   15-JAN-1991;   91US-0642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification,
PT   gene mapping, and selective breeding
XX
PS   Table 7; Page 157; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between
CC   250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC   One out of 50 clones cross-hybridised.  Assuming independent
CC   distribution of microsatellites and MboI sites, the frequency of
CC   (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC   000.  The sequence information for ca. 230 such bovine microsatellites
CC   is summarised in the specification and indexed herein (see below).
CC   The sequences upstream and downstream of the microsatellite sequence
CC   were used to generate the required PCR primers for in vitro
CC   amplification of the corresp. microsatellite (using the program
CC   OPTIPRIM).  The microsatellites may be used to identify individuals,
CC   for parentage testing, and in the genetic mapping of economic trait
CC   loci, or genes involved the determinism of economically important
CC   traits esp. in cattle, to allow selective breeding.
CC   See also AAQ33501-34437.
XX
SQ   Sequence 46 BP; 18 A; 2 C; 26 G; 0 U; 0 other;

  Query Match             1.7%;  Score 26.8;  DB 13;  Length 46;
  Best Local Similarity   73.9%;  Pred. No. 5.8e+04;
  Matches   34;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy     24 AGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGAG 69
          || ||| ||| |||| |||| | || || || || |  ||||||||
Db      1 AGAGAGAGGGAGAGCGGGAGAGCGGGAGAGAGAGAGAGAGAGAG 46


RESULT 25
AAF60024
ID   AAF60024 standard; DNA; 45 BP.
XX
AC   AAF60024;
XX
DT   26-APR-2001  (first entry)
XX
DE   DNA linker.
XX
KW   Antibody; sperm; S19; contraception; ss.
XX
OS   Synthetic.
XX
PN   WO200107083-A1.
XX
PD   01-FEB-2001.
XX
PF   21-JUL-2000; 2000WO-US19843.
XX
PR   23-JUL-1999;   99US-0145512.
XX
PA   (UYVI-) UNIV VIRGINIA PATENT FOUND.
XX
PI   Herr JC,  Norton EJ,  Diekman AB;
XX
DR   WPI; 2001-182730/18.
```

XX
PT New recombinant antibody derivative of monoclonal antibody S19, useful
PT as a reagent for purifying or detecting human spermatozoa, as an active
PT ingredient of a spermistatic agent, or as a component of a spermicidal
PT contraceptive -
XX
PS Disclosure; Page 43; 48pp; English.
XX
CC The present invention relates to a recombinant antibody capable of
CC specifically binding to sperm agglutination antigen-1 (SAGA-1).
CC The recombinant antibody has two peptide fragments of the S19
CC antibody and the fragments are joined together by a linker.
CC The recombinant monoclonal antibodies are useful in a passive
CC immunity composition for contraception as they inhibit the ability of
CC sperm to fertilize an egg. The antibodies may be used e.g. as an
CC active ingredient of a spermistatic agent, or as a component of a
CC spermicidal contraceptive.
XX
SQ Sequence 45 BP; 2 A; 10 C; 27 G; 6 T; 0 other;

Query Match 1.7%; Score 26.4; DB 22; Length 45;
Best Local Similarity 75.0%; Pred. No. 6.8e+04;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
Qy    1341 GCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGC 1384
           ||||||| | |||||| || || |     ||||||||||| ||
Db       2 GCGGCGGCGGCAGCGGTGGTGGTGGTTCTGGGGGCGGCGGCAGC 45
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Search completed: March 13, 2003, 21:59:12
Job time : 426 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 13, 2003, 21:52:28 ; Search time 72 Seconds
(without alignments)
6712.814 Million cell updates/sec

Title: US-10-001-844-3
Perfect score: 1576
Sequence: 1 gcgaggcagccagcgaggga.....gaggggcgcgggaggggcc 1576

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_NA:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	36	2.3	49	4	US-09-325-256-31	Sequence 31, Appl
	2	28.2	1.8	50	4	US-09-930-181-14	Sequence 14, Appl
	3	26	1.6	50	4	US-09-580-923-35	Sequence 35, Appl
	4	25	1.6	33	1	US-08-068-747-7	Sequence 7, Appli
	5	24.6	1.6	50	3	US-08-846-020A-6	Sequence 6, Appli
	6	24.6	1.6	50	4	US-09-617-871-6	Sequence 6, Appli
	7	24	1.5	24	1	US-08-748-591-11	Sequence 11, Appl
	8	24	1.5	24	2	US-08-356-060A-43	Sequence 43, Appl
	9	24	1.5	24	4	US-08-460-900C-43	Sequence 43, Appl
	10	24	1.5	24	4	US-08-674-509B-43	Sequence 43, Appl
	11	24	1.5	24	4	US-08-954-698-43	Sequence 43, Appl
	12	24	1.5	24	4	US-08-957-874-43	Sequence 43, Appl
	13	24	1.5	45	1	US-08-258-026A-13	Sequence 13, Appl
	14	24	1.5	45	4	US-09-813-781-129	Sequence 129, App
	15	24	1.5	45	5	PCT-US95-07541-13	Sequence 13, Appl
c	16	23.6	1.5	30	1	US-08-068-747-2	Sequence 2, Appli
	17	23.6	1.5	38	4	US-09-499-884-12	Sequence 12, Appl
	18	23.6	1.5	48	4	US-09-497-933A-19	Sequence 19, Appl
	19	23.6	1.5	50	4	US-09-930-181-13	Sequence 13, Appl
c	20	23.4	1.5	25	1	US-08-748-591-12	Sequence 12, Appl
c	21	22.4	1.4	32	4	US-09-083-123-5	Sequence 5, Appli
	22	22	1.4	47	4	US-09-325-256-30	Sequence 30, Appl
	23	21.8	1.4	35	1	US-08-340-045-7	Sequence 7, Appli
	24	21.8	1.4	35	3	US-08-871-302A-7	Sequence 7, Appli
	25	21.6	1.4	40	4	US-09-485-737B-5	Sequence 5, Appli
c	26	21.4	1.4	31	4	US-09-083-123-4	Sequence 4, Appli
	27	21.4	1.4	50	4	US-09-165-264-4	Sequence 4, Appli
	28	21.2	1.3	49	4	US-09-183-866-7	Sequence 7, Appli
	29	21	1.3	47	4	US-09-641-638-935	Sequence 935, App
	30	21	1.3	47	4	US-09-641-638-1096	Sequence 1096, Ap
c	31	21	1.3	50	1	US-08-171-389-374	Sequence 374, App
c	32	21	1.3	50	1	US-08-123-936-374	Sequence 374, App
c	33	21	1.3	50	2	US-08-475-228A-374	Sequence 374, App
c	34	21	1.3	50	3	US-08-482-080A-374	Sequence 374, App
c	35	21	1.3	50	4	US-09-354-947-374	Sequence 374, App
c	36	21	1.3	50	5	PCT-US93-12388-374	Sequence 374, App
	37	20.8	1.3	47	4	US-09-641-638-934	Sequence 934, App
c	38	20.8	1.3	48	3	US-08-478-097A-33	Sequence 33, Appl
	39	20.8	1.3	49	4	US-09-538-709-1159	Sequence 1159, Ap
c	40	20.6	1.3	45	1	US-07-885-689A-2	Sequence 2, Appli
	41	20.6	1.3	45	4	US-08-487-761-1	Sequence 1, Appli
c	42	20.6	1.3	45	4	US-09-497-933A-22	Sequence 22, Appl
	43	20.6	1.3	48	2	US-08-750-128-2	Sequence 2, Appli
c	44	20.4	1.3	30	4	US-09-083-123-2	Sequence 2, Appli
	45	20.4	1.3	30	4	US-09-083-123-8	Sequence 8, Appli
c	46	20.4	1.3	40	4	US-09-677-045-10	Sequence 10, Appl
	47	20.4	1.3	41	3	US-08-930-589A-14	Sequence 14, Appl
	48	20.4	1.3	41	4	US-09-599-781-14	Sequence 14, Appl
	49	20.4	1.3	44	3	US-08-846-020A-5	Sequence 5, Appli
	50	20.4	1.3	44	4	US-09-617-871-5	Sequence 5, Appli
c	51	20.4	1.3	47	5	PCT-US95-04439-7	Sequence 7, Appli
c	52	20.4	1.3	49	4	US-09-538-709-1141	Sequence 1141, Ap
	53	20.4	1.3	50	4	US-09-165-264-3	Sequence 3, Appli
	54	20.2	1.3	42	4	US-09-162-484-7	Sequence 7, Appli
	55	20.2	1.3	46	1	US-08-171-389-85	Sequence 85, Appl
	56	20.2	1.3	46	1	US-08-123-936-85	Sequence 85, Appl
	57	20.2	1.3	46	2	US-08-475-228A-85	Sequence 85, Appl
	58	20.2	1.3	46	3	US-08-482-080A-85	Sequence 85, Appl
	59	20.2	1.3	46	4	US-09-354-947-85	Sequence 85, Appl
	60	20.2	1.3	46	5	PCT-US93-12388-85	Sequence 85, Appl
c	61	20.2	1.3	47	2	US-08-975-902-48	Sequence 48, Appl
c	62	20.2	1.3	47	3	US-09-251-565-48	Sequence 48, Appl
	63	20.2	1.3	48	4	US-09-198-956-26	Sequence 26, Appl
	64	20.2	1.3	48	4	US-09-198-955A-32	Sequence 32, Appl
	65	20.2	1.3	48	4	US-09-694-531-32	Sequence 32, Appl
	66	20.2	1.3	48	4	US-09-670-141-26	Sequence 26, Appl
c	67	20	1.3	42	3	US-08-448-619-4	Sequence 4, Appli
c	68	20	1.3	42	4	US-09-162-484-7	Sequence 7, Appli
	69	20	1.3	45	1	US-08-167-939A-14	Sequence 14, Appl
	70	20	1.3	45	1	US-08-567-538-14	Sequence 14, Appl
	71	20	1.3	45	4	US-09-561-490E-35	Sequence 35, Appl
c	72	20	1.3	50	1	US-08-672-571A-13	Sequence 13, Appl
c	73	19.6	1.2	42	4	US-08-933-219B-20	Sequence 20, Appl
c	74	19.6	1.2	42	4	US-09-321-481-20	Sequence 20, Appl
	75	19.6	1.2	50	1	US-07-972-032-75	Sequence 75, Appl
c	76	19.4	1.2	33	1	US-07-723-002C-13	Sequence 13, Appl
	77	19.4	1.2	39	4	US-09-325-256-27	Sequence 27, Appl
	78	19.4	1.2	42	4	US-09-325-256-29	Sequence 29, Appl
	79	19.4	1.2	43	4	US-09-042-353-395	Sequence 395, App
	80	19.4	1.2	43	4	US-08-758-417A-245	Sequence 245, App
	81	19.4	1.2	45	3	US-08-718-904-50	Sequence 50, Appl
	82	19.4	1.2	45	5	PCT-US95-10973A-43	Sequence 43, Appl
	83	19.4	1.2	46	4	US-09-390-867A-49	Sequence 49, Appl
	84	19.4	1.2	46	4	US-09-548-260-49	Sequence 49, Appl
	85	19.2	1.2	36	4	US-08-026-143B-28	Sequence 28, Appl
	86	19.2	1.2	36	5	PCT-US92-10621-28	Sequence 28, Appl
	87	19.2	1.2	36	5	PCT-US94-02233-28	Sequence 28, Appl
c	88	19.2	1.2	42	1	US-07-803-633A-8	Sequence 8, Appli
c	89	19.2	1.2	42	2	US-08-525-742-18	Sequence 18, Appl
	90	19.2	1.2	44	1	US-08-222-177A-385	Sequence 385, App
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c	92	19.2	1.2	45	5	PCT-US95-07541-14	Sequence 14, Appl
	93	19.2	1.2	46	4	US-08-795-876-8	Sequence 8, Appli
c	94	19.2	1.2	47	2	US-08-406-855A-10	Sequence 10, Appl
c	95	19.2	1.2	47	3	US-09-206-899-10	Sequence 10, Appl
c	96	19.2	1.2	47	4	US-09-688-415-15	Sequence 15, Appl
	97	19.2	1.2	48	1	US-08-229-284A-11	Sequence 11, Appl
c	98	19.2	1.2	48	1	US-08-023-757-5	Sequence 5, Appli
c	99	19.2	1.2	48	1	US-08-177-502-5	Sequence 5, Appli
c	100	19.2	1.2	48	2	US-08-383-621-8	Sequence 8, Appli

c 101	19.2	1.2	48	3	US-08-459-906-8	Sequence 8, Appli
c 102	19.2	1.2	49	1	US-08-171-389-405	Sequence 405, App
c 103	19.2	1.2	49	1	US-08-123-936-405	Sequence 405, App
c 104	19.2	1.2	49	2	US-08-475-228A-405	Sequence 405, App
c 105	19.2	1.2	49	3	US-08-482-080A-405	Sequence 405, App
c 106	19.2	1.2	49	4	US-09-354-947-405	Sequence 405, App
c 107	19.2	1.2	49	5	PCT-US93-12388-405	Sequence 405, App
108	19.2	1.2	50	1	US-08-644-729-12	Sequence 12, Appl
c 109	19	1.2	19	1	US-08-748-591-16	Sequence 16, Appl
c 110	19	1.2	19	1	US-08-748-591-21	Sequence 21, Appl
111	19	1.2	19	4	US-09-102-491-5	Sequence 5, Appli
112	19	1.2	19	4	US-09-102-491-9	Sequence 9, Appli
c 113	19	1.2	30	4	US-09-813-781-11	Sequence 11, Appl
c 114	19	1.2	30	4	US-09-813-781-13	Sequence 13, Appl
c 115	19	1.2	36	4	US-09-301-199A-2	Sequence 2, Appli
116	19	1.2	39	4	US-09-450-072-8	Sequence 8, Appli
117	19	1.2	39	4	US-09-351-348-8	Sequence 8, Appli
c 118	19	1.2	41	4	US-08-646-265A-105	Sequence 105, App
c 119	19	1.2	41	4	US-08-327-874A-32	Sequence 32, Appl
c 120	19	1.2	41	5	PCT-US94-09700-32	Sequence 32, Appl
121	19	1.2	45	2	US-08-436-664-13	Sequence 13, Appl
c 122	19	1.2	45	2	US-08-436-664-14	Sequence 14, Appl
123	19	1.2	45	3	US-09-135-642-13	Sequence 13, Appl
c 124	19	1.2	45	3	US-09-135-642-14	Sequence 14, Appl
125	19	1.2	45	3	US-08-394-232A-13	Sequence 13, Appl
c 126	19	1.2	45	3	US-08-394-232A-14	Sequence 14, Appl
c 127	19	1.2	45	4	US-09-813-781-7	Sequence 7, Appli
128	19	1.2	45	5	PCT-US95-04080-13	Sequence 13, Appl
c 129	19	1.2	45	5	PCT-US95-04080-14	Sequence 14, Appl
130	19	1.2	46	2	US-08-448-418-10	Sequence 10, Appl
c 131	18.8	1.2	39	4	US-09-450-072-8	Sequence 8, Appli
c 132	18.8	1.2	39	4	US-09-351-348-8	Sequence 8, Appli
133	18.8	1.2	40	2	US-08-790-963-75	Sequence 75, Appl
134	18.8	1.2	40	4	US-09-371-774-75	Sequence 75, Appl
135	18.8	1.2	44	2	US-08-403-852D-35	Sequence 35, Appl
136	18.8	1.2	44	3	US-08-510-646B-37	Sequence 37, Appl
137	18.8	1.2	44	4	US-09-231-818-35	Sequence 35, Appl
c 138	18.8	1.2	47	2	US-08-790-963-56	Sequence 56, Appl
c 139	18.8	1.2	47	4	US-09-371-774-56	Sequence 56, Appl
140	18.8	1.2	48	1	US-08-629-600-2	Sequence 2, Appli
141	18.8	1.2	48	4	US-09-076-761-2	Sequence 2, Appli
142	18.8	1.2	48	4	US-09-538-709-82	Sequence 82, Appl
143	18.8	1.2	48	4	US-09-538-709-1249	Sequence 1249, Ap
144	18.8	1.2	49	4	US-09-538-709-989	Sequence 989, App
145	18.8	1.2	49	4	US-09-538-709-1010	Sequence 1010, Ap
146	18.8	1.2	49	4	US-09-538-709-1158	Sequence 1158, Ap
c 147	18.8	1.2	50	4	US-09-455-679-17	Sequence 17, Appl
148	18.6	1.2	25	1	US-08-374-144-3	Sequence 3, Appli
149	18.6	1.2	25	1	US-08-775-164-3	Sequence 3, Appli
150	18.6	1.2	25	2	US-08-775-609-3	Sequence 3, Appli
151	18.6	1.2	25	2	US-08-775-607-3	Sequence 3, Appli
152	18.6	1.2	25	5	PCT-US93-06828-3	Sequence 3, Appli
153	18.6	1.2	44	2	US-08-595-043A-45	Sequence 45, Appl
154	18.6	1.2	45	3	US-08-444-818-249	Sequence 249, App
155	18.6	1.2	45	4	US-09-561-490E-37	Sequence 37, Appl
c 156	18.6	1.2	46	2	US-08-263-911-19	Sequence 19, Appl
157	18.6	1.2	47	4	US-09-641-638-968	Sequence 968, App
158	18.6	1.2	48	2	US-08-750-128-8	Sequence 8, Appli
c 159	18.6	1.2	49	1	US-07-972-032-74	Sequence 74, Appl
c 160	18.6	1.2	49	1	US-08-642-255-87	Sequence 87, Appl
c 161	18.6	1.2	49	4	US-09-538-709-112	Sequence 112, App
162	18.6	1.2	49	4	US-09-538-709-1009	Sequence 1009, Ap
c 163	18.6	1.2	49	4	US-09-538-709-1279	Sequence 1279, Ap
c 164	18.6	1.2	50	1	US-08-171-389-463	Sequence 463, App
c 165	18.6	1.2	50	1	US-08-123-936-463	Sequence 463, App
c 166	18.6	1.2	50	2	US-08-475-228A-463	Sequence 463, App
c 167	18.6	1.2	50	3	US-08-482-080A-463	Sequence 463, App
c 168	18.6	1.2	50	4	US-08-785-668-23	Sequence 23, Appl
c 169	18.6	1.2	50	4	US-09-354-947-463	Sequence 463, App
c 170	18.6	1.2	50	5	PCT-US93-12388-463	Sequence 463, App
c 171	18.4	1.2	43	2	US-08-465-473B-27	Sequence 27, Appl
172	18.4	1.2	44	2	US-08-982-232-17	Sequence 17, Appl
173	18.4	1.2	45	1	US-08-440-391-31	Sequence 31, Appl
174	18.4	1.2	45	2	US-08-908-597A-31	Sequence 31, Appl
175	18.4	1.2	45	4	US-09-236-385A-31	Sequence 31, Appl
176	18.4	1.2	45	5	PCT-US96-06122-31	Sequence 31, Appl
c 177	18.4	1.2	47	1	US-08-334-177-9	Sequence 9, Appli
178	18.4	1.2	47	4	US-08-785-668-20	Sequence 20, Appl
c 179	18.4	1.2	47	4	US-08-785-668-21	Sequence 21, Appl
c 180	18.4	1.2	47	5	PCT-US95-13830-9	Sequence 9, Appli
c 181	18.4	1.2	48	5	PCT-US94-06079-32	Sequence 32, Appl
182	18.4	1.2	49	1	US-08-171-389-405	Sequence 405, App
183	18.4	1.2	49	1	US-08-123-936-405	Sequence 405, App
184	18.4	1.2	49	2	US-08-475-228A-405	Sequence 405, App
185	18.4	1.2	49	3	US-08-482-080A-405	Sequence 405, App
186	18.4	1.2	49	4	US-09-354-947-405	Sequence 405, App
187	18.4	1.2	49	4	US-09-538-709-930	Sequence 930, App
c 188	18.4	1.2	49	4	US-09-538-709-1153	Sequence 1153, Ap
189	18.4	1.2	49	5	PCT-US93-12388-405	Sequence 405, App
c 190	18.4	1.2	50	1	US-08-171-389-126	Sequence 126, App
191	18.4	1.2	50	1	US-08-171-389-481	Sequence 481, App
c 192	18.4	1.2	50	1	US-08-123-936-126	Sequence 126, App
193	18.4	1.2	50	1	US-08-123-936-481	Sequence 481, App
c 194	18.4	1.2	50	2	US-08-475-228A-126	Sequence 126, App
195	18.4	1.2	50	2	US-08-475-228A-481	Sequence 481, App
c 196	18.4	1.2	50	3	US-08-482-080A-126	Sequence 126, App
197	18.4	1.2	50	3	US-08-482-080A-481	Sequence 481, App
c 198	18.4	1.2	50	4	US-09-354-947-126	Sequence 126, App
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c 200	18.4	1.2	50	5	PCT-US93-12388-126	Sequence 126, App
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207	18.2	1.2	39	2	US-08-596-387B-37	Sequence 37, Appl
208	18.2	1.2	39	4	US-09-067-615-37	Sequence 37, Appl
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c 211	18.2	1.2	40	2	US-08-050-478-114	Sequence 114, App
c 212	18.2	1.2	40	4	US-09-414-117-114	Sequence 114, App
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221	18.2	1.2	46	3	US-08-482-080A-184	Sequence 184, App
222	18.2	1.2	46	4	US-09-354-947-184	Sequence 184, App
223	18.2	1.2	46	5	PCT-US93-12388-184	Sequence 184, App
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234	18.2	1.2	49	4	US-09-538-709-1060	Sequence 1060, Ap
235	18.2	1.2	50	1	US-08-171-389-331	Sequence 331, App
236	18.2	1.2	50	1	US-08-123-936-331	Sequence 331, App
237	18.2	1.2	50	2	US-08-475-228A-331	Sequence 331, App
238	18.2	1.2	50	3	US-08-482-080A-331	Sequence 331, App
c 239	18.2	1.2	50	4	US-09-198-723A-90	Sequence 90, Appl
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241	18.2	1.2	50	5	PCT-US93-12388-331	Sequence 331, App
c 242	18	1.1	18	4	US-09-102-491-6	Sequence 6, Appli
243	18	1.1	27	1	US-08-758-306-1170	Sequence 1170, Ap
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245	18	1.1	35	3	US-09-078-166-4	Sequence 4, Appli
246	18	1.1	35	4	US-08-997-467-4	Sequence 4, Appli

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	282	18	1.1	50	1	US-08-123-936-374
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Sequence 31, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 34, Appl
Sequence 28, Appl
Patent No. 5520913
Sequence 7, Appli
Sequence 22, Appl
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Sequence 23, Appl
Sequence 22, Appl
Sequence 17, Appl
Sequence 28, Appl
Sequence 16, Appl
Sequence 2, Appli
Sequence 11, Appl
Sequence 20, Appl
Sequence 18, Appl
Sequence 4, Appli
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Sequence 1074, Ap
Sequence 203, App
Sequence 203, App
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Sequence 203, App
Sequence 37, Appl
Sequence 37, Appl
Sequence 203, App
Sequence 203, App
Sequence 33, Appl
Sequence 955, App
Sequence 978, App
Sequence 374, App
Sequence 474, App
Sequence 169, App
Sequence 374, App
Sequence 474, App
Sequence 88, Appl
Sequence 374, App
Sequence 474, App
Sequence 33, Appl
Sequence 33, Appl
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Sequence 474, App
Sequence 33, Appl
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Sequence 5, Appli
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Sequence 14, Appl
Sequence 374, App
Sequence 474, App
Sequence 374, App
Sequence 474, App
Sequence 24, Appl
Sequence 10, Appl
Sequence 6, Appli
Sequence 291, App
Sequence 291, App
Sequence 15, Appl
Sequence 291, App
Sequence 291, App
Sequence 14, Appl
Sequence 15, Appl
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Sequence 28, Appl
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Sequence 31, Appl
Sequence 32, Appl
Sequence 30, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 537, App

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	336	17.6	1.1	36	5	PCT-US94-09700-28
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	339	17.6	1.1	41	1	US-08-123-936-243
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Sequence 537, App
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Sequence 269, App
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Sequence 269, App
Sequence 718, App
Sequence 1156, Ap
Sequence 14, Appl
Sequence 42, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 262, App
Sequence 262, App
Sequence 262, App
Sequence 262, App
Sequence 262, App
Sequence 102, App
Sequence 1269, Ap
Sequence 262, App
Sequence 524, App
Sequence 591, App
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Sequence 591, App
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	427	17.4	1.1	44	1	US-08-171-389-152
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c	441	17.4	1.1	45	5	PCT-US93-12388-199
c	442	17.4	1.1	45	5	PCT-US94-06079-43
	443	17.4	1.1	46	1	US-08-235-503B-70
	444	17.4	1.1	46	5	PCT-US95-05265-70
	445	17.4	1.1	47	1	US-08-171-389-13
	446	17.4	1.1	47	1	US-08-123-936-13
	447	17.4	1.1	47	2	US-08-475-228A-13
	448	17.4	1.1	47	3	US-08-482-080A-13
	449	17.4	1.1	47	4	US-09-354-947-13
c	450	17.4	1.1	47	4	US-09-641-638-1078
	451	17.4	1.1	47	4	US-09-641-638-1186
	452	17.4	1.1	47	5	PCT-US93-12388-13
c	453	17.4	1.1	48	2	US-08-750-128-8
	454	17.4	1.1	48	3	US-08-755-587-197
	455	17.4	1.1	49	1	US-08-261-660A-27
	456	17.4	1.1	49	4	US-09-280-909A-27
	457	17.4	1.1	49	5	PCT-US94-06931-27
	458	17.4	1.1	50	1	US-08-357-399-11
	459	17.4	1.1	50	1	US-08-357-666-11
	460	17.4	1.1	50	1	US-08-206-175-11
	461	17.4	1.1	50	4	US-09-025-769B-117
	462	17.4	1.1	50	5	PCT-US91-03540A-5
	463	17.4	1.1	50	6	5168050-14
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c	465	17.2	1.1	24	4	US-09-226-683-31

Sequence 17, Appl
Sequence 17, Appl
Sequence 39, Appl
Sequence 524, App
Sequence 591, App
Sequence 78, Appl
Sequence 24, Appl
Sequence 39, Appl
Sequence 78, Appl
Sequence 5, Appli
Sequence 524, App
Sequence 591, App
Patent No. 5168050
Sequence 1, Appli
Sequence 80, Appl
Sequence 81, Appl
Sequence 2, Appli
Sequence 2, Appli
Patent No. 5256770
Sequence 8, Appli
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Sequence 876, App
Sequence 9, Appli
Sequence 12, Appl
Sequence 12, Appl
Sequence 24, Appl
Sequence 12, Appl
Sequence 28, Appl
Sequence 35, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 152, App
Sequence 152, App
Sequence 152, App
Sequence 152, App
Sequence 152, App
Sequence 152, App
Sequence 2, Appli
Sequence 199, App
Sequence 199, App
Sequence 199, App
Sequence 199, App
Sequence 7, Appli
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Sequence 199, App
Sequence 199, App
Sequence 43, Appl
Sequence 70, Appl
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Sequence 13, Appl
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Sequence 1078, Ap
Sequence 1186, Ap
Sequence 13, Appl
Sequence 8, Appli
Sequence 197, App
Sequence 27, Appl
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Sequence 117, App
Sequence 5, Appli
Patent No. 5168050
Sequence 31, Appl
Sequence 31, Appl

	466	17.2	1.1	24	4	US-09-387-699-12
c	467	17.2	1.1	24	4	US-09-035-183-31
	468	17.2	1.1	24	4	US-09-641-259B-12
c	469	17.2	1.1	30	4	US-09-052-919-21
	470	17.2	1.1	30	4	US-09-674-460-2
c	471	17.2	1.1	35	4	US-09-194-613-7
	472	17.2	1.1	36	4	US-09-423-439-39
	473	17.2	1.1	37	3	US-08-428-616A-3
c	474	17.2	1.1	38	4	US-08-966-341-5
	475	17.2	1.1	38	4	US-08-966-341-6
	476	17.2	1.1	39	4	US-09-183-866-5
c	477	17.2	1.1	39	4	US-09-517-871-16
c	478	17.2	1.1	40	1	US-07-612-673-16
	479	17.2	1.1	40	1	US-08-030-731A-26
c	480	17.2	1.1	40	1	US-08-539-666-17
	481	17.2	1.1	41	1	US-08-453-956-22
	482	17.2	1.1	41	1	US-08-086-631-22
	483	17.2	1.1	41	2	US-08-452-930-22
	484	17.2	1.1	41	5	PCT-US93-08174-22
c	485	17.2	1.1	42	2	US-08-124-981A-11
	486	17.2	1.1	42	3	US-08-827-974-1
c	487	17.2	1.1	42	3	US-09-037-190-9
c	488	17.2	1.1	42	3	US-09-037-192-9
c	489	17.2	1.1	42	3	US-09-037-143-9
c	490	17.2	1.1	42	4	US-09-049-691-9
c	491	17.2	1.1	42	4	US-08-260-174-9
	492	17.2	1.1	42	4	US-08-910-722-5
c	493	17.2	1.1	42	4	US-09-338-128A-9
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	496	17.2	1.1	42	5	PCT-US95-11405-18
	497	17.2	1.1	42	6	5182196-21
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c	501	17.2	1.1	45	4	US-08-487-761-1
	502	17.2	1.1	45	4	US-09-517-871-15
	503	17.2	1.1	45	5	PCT-US94-14106-15
	504	17.2	1.1	46	1	US-08-171-389-183
	505	17.2	1.1	46	1	US-08-123-936-183
	506	17.2	1.1	46	2	US-08-475-228A-183
	507	17.2	1.1	46	3	US-08-482-080A-183
	508	17.2	1.1	46	4	US-09-354-947-183
	509	17.2	1.1	46	5	PCT-US93-12388-183
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	523	17.2	1.1	49	1	US-08-086-634-10
	524	17.2	1.1	49	4	US-09-538-709-92
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c	528	17.2	1.1	50	1	US-08-123-936-112
c	529	17.2	1.1	50	1	US-08-123-936-331
c	530	17.2	1.1	50	2	US-08-475-228A-112
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c	534	17.2	1.1	50	4	US-09-455-679-16
c	535	17.2	1.1	50	4	US-09-354-947-112
c	536	17.2	1.1	50	4	US-09-354-947-331
c	537	17.2	1.1	50	5	PCT-US93-12388-112
c	538	17.2	1.1	50	5	PCT-US93-12388-331

Sequence 12, Appl
Sequence 31, Appl
Sequence 12, Appl
Sequence 21, Appl
Sequence 2, Appli
Sequence 7, Appli
Sequence 39, Appl
Sequence 3, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 16, Appl
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Sequence 18, Appl
Patent No. 5182196
Sequence 34, Appl
Sequence 34, Appl
Sequence 28, Appl
Sequence 1, Appli
Sequence 15, Appl
Sequence 15, Appl
Sequence 183, App
Sequence 183, App
Sequence 183, App
Sequence 183, App
Sequence 183, App
Sequence 183, App
Sequence 6, Appli
Sequence 786, App
Sequence 866, App
Sequence 1111, Ap
Sequence 1197, Ap
Sequence 1276, Ap
Sequence 14, Appl
Sequence 14, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 31, Appl
Sequence 10, Appl
Sequence 92, Appl
Sequence 1259, Ap
Sequence 112, App
Sequence 331, App
Sequence 112, App
Sequence 331, App
Sequence 112, App
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Sequence 112, App
Sequence 331, App
Sequence 16, Appl
Sequence 112, App
Sequence 331, App
Sequence 112, App
Sequence 331, App

	539	17	1.1	25	4	US-09-292-036-5
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	542	17	1.1	33	3	US-08-873-709-12
c	543	17	1.1	33	3	US-08-930-589A-15
	544	17	1.1	33	4	US-09-437-034B-7
	545	17	1.1	33	4	US-09-255-464B-8
c	546	17	1.1	33	4	US-09-599-781-15
c	547	17	1.1	33	5	PCT-US94-06331A-51
	548	17	1.1	35	3	US-08-463-903-40
c	549	17	1.1	35	4	US-08-810-009-65
	550	17	1.1	35	4	US-07-935-695-40
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c	553	17	1.1	37	3	US-08-873-709-11
	554	17	1.1	37	4	US-07-875-790B-10
c	555	17	1.1	37	4	US-09-437-034B-6
c	556	17	1.1	37	4	US-09-255-464B-7
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c	558	17	1.1	37	4	US-09-417-418-2
	559	17	1.1	38	1	US-08-707-793A-10
	560	17	1.1	38	1	US-08-707-792A-10
c	561	17	1.1	38	2	US-08-124-981A-21
c	562	17	1.1	38	3	US-09-037-190-19
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c	564	17	1.1	38	3	US-09-037-143-19
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c	566	17	1.1	38	4	US-08-260-174-19
c	567	17	1.1	38	4	US-09-338-128A-19
c	568	17	1.1	38	4	US-09-232-346-19
c	569	17	1.1	38	4	US-09-037-192-19
	570	17	1.1	39	4	US-08-556-978B-64
c	571	17	1.1	39	4	US-08-556-978B-65
	572	17	1.1	40	2	US-08-425-684-128
	573	17	1.1	40	2	US-08-675-502-128
c	574	17	1.1	40	4	US-09-546-483-1
c	575	17	1.1	40	4	US-09-823-177-1
	576	17	1.1	41	1	US-08-481-003-9
	577	17	1.1	41	3	US-08-485-598-9
c	578	17	1.1	42	1	US-08-468-036-30
c	579	17	1.1	42	2	US-08-376-843-30
	580	17	1.1	42	4	US-09-459-958-12
c	581	17	1.1	43	4	US-09-387-300-35
c	582	17	1.1	45	1	US-08-481-003-8
c	583	17	1.1	45	3	US-08-997-918-22
c	584	17	1.1	45	3	US-08-485-598-8
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	586	17	1.1	45	4	US-09-518-914-14
c	587	17	1.1	46	1	US-07-854-596B-10
	588	17	1.1	46	1	US-08-171-389-175
	589	17	1.1	46	1	US-08-123-936-175
	590	17	1.1	46	2	US-08-475-228A-175
	591	17	1.1	46	2	US-07-916-098A-60
	592	17	1.1	46	3	US-08-482-080A-175
	593	17	1.1	46	4	US-09-354-947-175
	594	17	1.1	46	5	PCT-US93-12388-175
c	595	17	1.1	47	4	US-09-641-638-1190
	596	17	1.1	48	4	US-08-828-533-37
	597	17	1.1	49	1	US-07-994-469A-26
	598	17	1.1	49	4	US-09-538-709-929
	599	17	1.1	49	4	US-09-538-709-940
	600	17	1.1	49	4	US-09-538-709-1051
	601	17	1.1	49	4	US-09-538-709-1097
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c	605	17	1.1	50	1	US-08-123-936-364
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c	607	17	1.1	50	2	US-08-475-228A-364
c	608	17	1.1	50	2	US-08-475-228A-497
c	609	17	1.1	50	3	US-08-482-080A-364
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c	611	17	1.1	50	3	US-08-998-099-286

Sequence 5, Appli
Sequence 12, Appl
Sequence 3, Appli
Sequence 12, Appl
Sequence 15, Appl
Sequence 7, Appli
Sequence 8, Appli
Sequence 15, Appl
Sequence 51, Appl
Sequence 40, Appl
Sequence 65, Appl
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Sequence 11, Appl
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Sequence 19, Appl
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Sequence 64, Appl
Sequence 65, Appl
Sequence 128, App
Sequence 128, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 30, Appl
Sequence 30, Appl
Sequence 12, Appl
Sequence 35, Appl
Sequence 8, Appli
Sequence 22, Appl
Sequence 8, Appli
Sequence 784, App
Sequence 14, Appl
Sequence 10, Appl
Sequence 175, App
Sequence 175, App
Sequence 175, App
Sequence 60, Appl
Sequence 175, App
Sequence 175, App
Sequence 175, App
Sequence 1190, Ap
Sequence 37, Appl
Sequence 26, Appl
Sequence 929, App
Sequence 940, App
Sequence 1051, Ap
Sequence 1097, Ap
Sequence 36, Appl
Sequence 364, App
Sequence 497, App
Sequence 364, App
Sequence 497, App
Sequence 364, App
Sequence 497, App
Sequence 364, App
Sequence 497, App
Sequence 286, App

c	612	17	1.1	50	4	US-09-128-354-17
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c	615	17	1.1	50	4	US-09-930-181-14
c	616	17	1.1	50	4	US-09-296-328A-22
c	617	17	1.1	50	4	US-09-538-709-1077
c	618	17	1.1	50	5	PCT-US93-12388-364
c	619	17	1.1	50	5	PCT-US93-12388-497
c	620	16.8	1.1	29	1	US-08-586-272-17
c	621	16.8	1.1	29	3	US-09-082-969-17
c	622	16.8	1.1	30	1	US-08-318-193-64
c	623	16.8	1.1	30	1	US-08-543-630-1
	624	16.8	1.1	30	2	US-08-888-366-28
c	625	16.8	1.1	30	4	US-08-460-900C-49
c	626	16.8	1.1	30	4	US-08-674-509B-19
c	627	16.8	1.1	30	4	US-08-954-698-19
	628	16.8	1.1	30	4	US-08-589-109A-13
	629	16.8	1.1	33	1	US-08-137-117D-75
c	630	16.8	1.1	33	1	US-08-137-117D-76
	631	16.8	1.1	33	1	US-08-436-717-75
c	632	16.8	1.1	33	1	US-08-436-717-76
c	633	16.8	1.1	33	4	US-08-753-247-3
c	634	16.8	1.1	35	3	US-08-685-871-15
c	635	16.8	1.1	35	3	US-08-685-871-20
c	636	16.8	1.1	35	3	US-08-685-871-24
c	637	16.8	1.1	35	3	US-08-685-871-28
c	638	16.8	1.1	35	3	US-08-685-871-34
c	639	16.8	1.1	35	3	US-08-685-871-36
c	640	16.8	1.1	35	3	US-08-685-871-38
c	641	16.8	1.1	35	3	US-08-685-871-46
c	642	16.8	1.1	35	3	US-08-685-871-48
	643	16.8	1.1	36	1	US-08-455-627-7
	644	16.8	1.1	36	1	US-08-435-350-3
	645	16.8	1.1	36	2	US-08-689-856-7
c	646	16.8	1.1	36	4	US-09-689-291A-6
	647	16.8	1.1	37	1	US-08-428-733A-10
c	648	16.8	1.1	37	1	US-08-428-733A-45
	649	16.8	1.1	39	4	US-09-099-307-20
	650	16.8	1.1	40	1	US-08-390-878-3
	651	16.8	1.1	40	2	US-08-850-049-126
	652	16.8	1.1	40	2	US-08-050-478-126
	653	16.8	1.1	40	4	US-09-414-117-126
	654	16.8	1.1	40	4	US-09-678-437-126
	655	16.8	1.1	41	2	US-08-373-190-57
	656	16.8	1.1	41	2	US-08-438-190A-57
	657	16.8	1.1	41	3	US-09-287-145A-57
c	658	16.8	1.1	41	4	US-09-214-151-5
	659	16.8	1.1	41	4	US-09-556-111-57
c	660	16.8	1.1	42	3	US-08-874-825-6
c	661	16.8	1.1	42	3	US-08-663-824-6
	662	16.8	1.1	42	3	US-08-448-619-5
c	663	16.8	1.1	42	4	US-09-231-303-6
c	664	16.8	1.1	43	1	US-07-931-473B-263
c	665	16.8	1.1	43	1	US-07-714-131C-263
c	666	16.8	1.1	43	1	US-08-412-110-263
c	667	16.8	1.1	43	1	US-08-409-442A-263
c	668	16.8	1.1	43	2	US-08-469-609A-263
c	669	16.8	1.1	43	3	US-08-726-807B-23
c	670	16.8	1.1	43	3	US-09-143-190-263
c	671	16.8	1.1	43	3	US-09-258-367-23
c	672	16.8	1.1	43	4	US-09-546-550-23
c	673	16.8	1.1	43	4	US-09-431-414-23
c	674	16.8	1.1	43	4	US-09-225-670-23
c	675	16.8	1.1	43	4	US-09-502-344-263
c	676	16.8	1.1	43	4	US-09-431-349C-23
	677	16.8	1.1	44	2	US-08-982-232-2
	678	16.8	1.1	44	2	US-08-982-232-5
c	679	16.8	1.1	44	2	US-08-982-232-15
	680	16.8	1.1	44	3	US-09-219-849-23
c	681	16.8	1.1	44	3	US-09-219-849-24
	682	16.8	1.1	45	1	US-08-171-389-84
	683	16.8	1.1	45	1	US-08-449-207-3
	684	16.8	1.1	45	1	US-08-449-207-3

Sequence 17, Appl
Sequence 364, App
Sequence 497, App
Sequence 14, Appl
Sequence 22, Appl
Sequence 1077, Ap
Sequence 364, App
Sequence 497, App
Sequence 17, Appl
Sequence 17, Appl
Sequence 64, Appl
Sequence 1, Appli
Sequence 28, Appl
Sequence 49, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 13, Appl
Sequence 75, Appl
Sequence 76, Appl
Sequence 75, Appl
Sequence 76, Appl
Sequence 3, Appli
Sequence 15, Appl
Sequence 20, Appl
Sequence 24, Appl
Sequence 28, Appl
Sequence 34, Appl
Sequence 36, Appl
Sequence 38, Appl
Sequence 46, Appl
Sequence 48, Appl
Sequence 7, Appli
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Sequence 6, Appli
Sequence 10, Appl
Sequence 45, Appl
Sequence 20, Appl
Sequence 3, Appli
Sequence 126, App
Sequence 126, App
Sequence 126, App
Sequence 126, App
Sequence 57, Appl
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Sequence 263, App
Sequence 23, Appl
Sequence 2, Appli
Sequence 5, Appli
Sequence 15, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 84, Appl
Sequence 3, Appli
Sequence 3, Appli

685	16.8	1.1	45	1	US-08-123-936-84	Sequence 84, Appl
c 686	16.8	1.1	45	2	US-08-039-198B-3	Sequence 3, Appli
687	16.8	1.1	45	2	US-08-475-228A-84	Sequence 84, Appl
688	16.8	1.1	45	2	US-08-680-326-65	Sequence 65, Appl
689	16.8	1.1	45	2	US-08-350-260A-548	Sequence 548, App
c 690	16.8	1.1	45	2	US-08-982-232-1	Sequence 1, Appli
691	16.8	1.1	45	3	US-08-482-080A-84	Sequence 84, Appl
692	16.8	1.1	45	3	US-08-997-918-23	Sequence 23, Appl
c 693	16.8	1.1	45	3	US-09-371-710-40	Sequence 40, Appl
c 694	16.8	1.1	45	4	US-09-648-386-40	Sequence 40, Appl
695	16.8	1.1	45	4	US-09-354-947-84	Sequence 84, Appl
696	16.8	1.1	45	4	US-09-311-626B-56	Sequence 56, Appl
697	16.8	1.1	45	5	PCT-US93-12388-84	Sequence 84, Appl
698	16.8	1.1	45	5	PCT-US94-14106-13	Sequence 13, Appl
699	16.8	1.1	45	5	PCT-US94-14106-14	Sequence 14, Appl
700	16.8	1.1	45	5	PCT-US94-14106-16	Sequence 16, Appl
701	16.8	1.1	46	4	US-09-065-104-14	Sequence 14, Appl
702	16.8	1.1	46	4	US-09-198-603C-21	Sequence 21, Appl
c 703	16.8	1.1	46	4	US-08-795-876-9	Sequence 9, Appli
c 704	16.8	1.1	47	4	US-09-039-982A-28	Sequence 28, Appl
705	16.8	1.1	47	4	US-09-039-982A-29	Sequence 29, Appl
c 706	16.8	1.1	47	4	US-09-039-641-28	Sequence 28, Appl
707	16.8	1.1	47	4	US-09-039-641-29	Sequence 29, Appl
c 708	16.8	1.1	47	4	US-09-039-762A-28	Sequence 28, Appl
709	16.8	1.1	47	4	US-09-039-762A-29	Sequence 29, Appl
710	16.8	1.1	47	4	US-09-025-769B-106	Sequence 106, App
c 711	16.8	1.1	47	4	US-09-042-492D-28	Sequence 28, Appl
712	16.8	1.1	47	4	US-09-042-492D-29	Sequence 29, Appl
713	16.8	1.1	47	4	US-09-641-638-1184	Sequence 1184, Ap
714	16.8	1.1	47	4	US-09-641-638-1296	Sequence 1296, Ap
c 715	16.8	1.1	47	4	US-08-913-612A-28	Sequence 28, Appl
716	16.8	1.1	47	4	US-08-913-612A-29	Sequence 29, Appl
c 717	16.8	1.1	48	3	US-08-478-097A-39	Sequence 39, Appl
c 718	16.8	1.1	48	3	US-08-874-825-5	Sequence 5, Appli
c 719	16.8	1.1	48	3	US-08-663-824-5	Sequence 5, Appli
720	16.8	1.1	48	3	US-09-012-515A-7	Sequence 7, Appli
721	16.8	1.1	48	3	US-08-360-144A-7	Sequence 7, Appli
c 722	16.8	1.1	48	4	US-09-485-737B-43	Sequence 43, Appl
c 723	16.8	1.1	48	4	US-09-231-303-5	Sequence 5, Appli
724	16.8	1.1	48	4	US-09-012-504A-7	Sequence 7, Appli
725	16.8	1.1	48	5	PCT-US95-06722-7	Sequence 7, Appli
c 726	16.8	1.1	49	1	US-07-994-469A-31	Sequence 31, Appl
727	16.8	1.1	49	4	US-09-020-846-59	Sequence 59, Appl
728	16.8	1.1	49	4	US-09-538-709-1080	Sequence 1080, Ap
729	16.8	1.1	49	4	US-09-538-709-1165	Sequence 1165, Ap
c 730	16.8	1.1	50	1	US-08-171-389-375	Sequence 375, App
c 731	16.8	1.1	50	1	US-08-171-389-504	Sequence 504, App
c 732	16.8	1.1	50	1	US-08-123-936-375	Sequence 375, App
c 733	16.8	1.1	50	1	US-08-123-936-504	Sequence 504, App
734	16.8	1.1	50	1	US-08-477-254A-21	Sequence 21, Appl
735	16.8	1.1	50	2	US-08-472-576B-21	Sequence 21, Appl
736	16.8	1.1	50	2	US-08-428-734B-21	Sequence 21, Appl
c 737	16.8	1.1	50	2	US-08-475-228A-375	Sequence 375, App
c 738	16.8	1.1	50	2	US-08-475-228A-504	Sequence 504, App
c 739	16.8	1.1	50	2	US-08-749-852-39	Sequence 39, Appl
c 740	16.8	1.1	50	3	US-08-482-080A-375	Sequence 375, App
c 741	16.8	1.1	50	3	US-08-482-080A-504	Sequence 504, App
742	16.8	1.1	50	3	US-08-836-922-12	Sequence 12, Appl
c 743	16.8	1.1	50	4	US-08-628-747-23	Sequence 23, Appl
c 744	16.8	1.1	50	4	US-09-227-717-6	Sequence 6, Appli
745	16.8	1.1	50	4	US-08-713-556F-21	Sequence 21, Appl
746	16.8	1.1	50	4	US-09-128-354-17	Sequence 17, Appl
c 747	16.8	1.1	50	4	US-09-354-947-375	Sequence 375, App
c 748	16.8	1.1	50	4	US-09-354-947-504	Sequence 504, App
c 749	16.8	1.1	50	5	PCT-US93-12388-375	Sequence 375, App
c 750	16.8	1.1	50	5	PCT-US93-12388-504	Sequence 504, App
c 751	16.6	1.1	24	2	US-08-384-324-6	Sequence 6, Appli
c 752	16.6	1.1	24	5	PCT-US96-01473-6	Sequence 6, Appli
753	16.6	1.1	26	4	US-09-485-737B-57	Sequence 57, Appl
c 754	16.6	1.1	29	1	US-08-568-147B-8	Sequence 8, Appli
c 755	16.6	1.1	30	5	PCT-US95-07372-3	Sequence 3, Appli
756	16.6	1.1	31	4	US-09-516-357-8	Sequence 8, Appli
757	16.6	1.1	32	1	US-08-469-802B-28	Sequence 28, Appl
758	16.6	1.1	32	2	US-08-267-803B-46	Sequence 46, Appl
c 759	16.6	1.1	32	4	US-08-976-427-18	Sequence 18, Appl
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761	16.6	1.1	33	3	US-09-026-673-5	Sequence 5, Appli
c 762	16.6	1.1	33	4	US-08-974-549A-616	Sequence 616, App
763	16.6	1.1	33	4	US-09-527-236A-13	Sequence 13, Appl
764	16.6	1.1	33	4	US-09-480-142-5	Sequence 5, Appli
765	16.6	1.1	34	4	US-08-974-549A-482	Sequence 482, App
c 766	16.6	1.1	34	4	US-09-529-279-46	Sequence 46, Appl
767	16.6	1.1	36	3	US-08-707-399E-4	Sequence 4, Appli
768	16.6	1.1	36	5	PCT-US93-08479-7	Sequence 7, Appli
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770	16.6	1.1	38	4	US-09-042-353-326	Sequence 326, App
771	16.6	1.1	38	4	US-08-758-417A-174	Sequence 174, App
c 772	16.6	1.1	39	5	PCT-US93-05240-3	Sequence 3, Appli
773	16.6	1.1	39	6	5240848-9	Patent No. 5240848
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776	16.6	1.1	40	1	US-08-199-507B-15	Sequence 15, Appl
777	16.6	1.1	40	1	US-08-199-507B-27	Sequence 27, Appl
778	16.6	1.1	40	1	US-08-199-507B-30	Sequence 30, Appl
779	16.6	1.1	40	1	US-08-441-828-15	Sequence 15, Appl
780	16.6	1.1	40	1	US-08-441-828-27	Sequence 27, Appl
781	16.6	1.1	40	1	US-08-441-828-30	Sequence 30, Appl
782	16.6	1.1	41	3	US-09-167-354-4	Sequence 4, Appli
783	16.6	1.1	41	4	US-09-642-855-4	Sequence 4, Appli
784	16.6	1.1	41	4	US-09-642-514-4	Sequence 4, Appli
c 785	16.6	1.1	41	4	US-09-438-954-37	Sequence 37, Appl
c 786	16.6	1.1	42	1	US-08-411-777-3	Sequence 3, Appli
c 787	16.6	1.1	42	3	US-09-136-421-2	Sequence 2, Appli
c 788	16.6	1.1	42	3	US-09-057-088-3	Sequence 3, Appli
c 789	16.6	1.1	42	4	US-09-358-972-235	Sequence 235, App
c 790	16.6	1.1	42	4	US-09-210-896-10	Sequence 10, Appl
c 791	16.6	1.1	42	4	US-09-430-615-25	Sequence 25, Appl
792	16.6	1.1	43	1	US-08-391-259-9	Sequence 9, Appli
793	16.6	1.1	43	2	US-08-839-425-9	Sequence 9, Appli
c 794	16.6	1.1	43	4	US-08-983-564A-28	Sequence 28, Appl
c 795	16.6	1.1	44	4	US-09-042-353-376	Sequence 376, App
c 796	16.6	1.1	44	4	US-08-758-417A-226	Sequence 226, App
c 797	16.6	1.1	44	4	US-09-647-390-2	Sequence 2, Appli
c 798	16.6	1.1	45	2	US-08-588-201-9	Sequence 9, Appli
c 799	16.6	1.1	45	2	US-09-169-605-9	Sequence 9, Appli
800	16.6	1.1	45	2	US-08-157-185-11	Sequence 11, Appl
c 801	16.6	1.1	45	3	US-08-893-327-9	Sequence 9, Appli
802	16.6	1.1	45	3	US-08-858-003-22	Sequence 22, Appl
803	16.6	1.1	45	3	US-09-078-166-22	Sequence 22, Appl
804	16.6	1.1	45	3	US-08-281-526B-11	Sequence 11, Appl
805	16.6	1.1	45	4	US-08-997-467-22	Sequence 22, Appl
806	16.6	1.1	45	4	US-09-232-468A-5	Sequence 5, Appli
c 807	16.6	1.1	45	4	US-08-639-294-4	Sequence 4, Appli
c 808	16.6	1.1	45	4	US-09-210-896-8	Sequence 8, Appli
c 809	16.6	1.1	45	4	US-09-210-896-12	Sequence 12, Appl
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811	16.6	1.1	45	4	US-09-217-228-4	Sequence 4, Appli
812	16.6	1.1	45	4	US-09-450-790A-11	Sequence 11, Appl
813	16.6	1.1	45	4	US-09-332-837-11	Sequence 11, Appl
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c 815	16.6	1.1	46	1	US-08-122-433-12	Sequence 12, Appl
c 816	16.6	1.1	46	1	US-08-122-433-13	Sequence 13, Appl
c 817	16.6	1.1	46	1	US-08-123-936-188	Sequence 188, App
c 818	16.6	1.1	46	2	US-08-475-228A-188	Sequence 188, App
c 819	16.6	1.1	46	3	US-08-482-080A-188	Sequence 188, App
c 820	16.6	1.1	46	4	US-09-354-947-188	Sequence 188, App
c 821	16.6	1.1	46	5	PCT-US93-12388-188	Sequence 188, App
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c 823	16.6	1.1	47	1	US-08-196-103A-1	Sequence 1, Appli
c 824	16.6	1.1	47	1	US-08-357-396-1	Sequence 1, Appli
c 825	16.6	1.1	47	1	US-08-386-141-1	Sequence 1, Appli
826	16.6	1.1	47	4	US-09-538-709-129	Sequence 129, App
827	16.6	1.1	47	4	US-09-538-709-1296	Sequence 1296, Ap
c 828	16.6	1.1	48	1	US-08-478-039-2	Sequence 2, Appli
c 829	16.6	1.1	48	1	US-08-476-349A-2	Sequence 2, Appli
830	16.6	1.1	48	4	US-09-144-914-24	Sequence 24, Appl

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	832	16.6	1.1	49	4	US-09-318-448-29
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	835	16.6	1.1	49	4	US-09-538-709-966
	836	16.6	1.1	49	4	US-09-538-709-976
	837	16.6	1.1	49	4	US-09-538-709-987
c	838	16.6	1.1	49	4	US-09-538-709-987
	839	16.6	1.1	49	4	US-09-538-709-1011
	840	16.6	1.1	49	4	US-09-538-709-1073
c	841	16.6	1.1	50	1	US-08-171-389-495
	842	16.6	1.1	50	1	US-08-171-389-571
c	843	16.6	1.1	50	1	US-08-123-936-495
	844	16.6	1.1	50	1	US-08-123-936-571
	845	16.6	1.1	50	1	US-08-416-756A-9
c	846	16.6	1.1	50	2	US-08-475-228A-495
	847	16.6	1.1	50	2	US-08-475-228A-571
c	848	16.6	1.1	50	2	US-08-793-170-18
c	849	16.6	1.1	50	3	US-08-482-080A-495
	850	16.6	1.1	50	3	US-08-482-080A-571
c	851	16.6	1.1	50	3	US-08-892-873-18
c	852	16.6	1.1	50	3	US-08-846-020A-6
c	853	16.6	1.1	50	4	US-09-334-765A-18
c	854	16.6	1.1	50	4	US-09-356-575E-18
	855	16.6	1.1	50	4	US-09-025-769B-345
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	857	16.6	1.1	50	4	US-09-025-769B-347
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	861	16.6	1.1	50	4	US-09-660-552-1
c	862	16.6	1.1	50	4	US-09-358-036-40
	863	16.6	1.1	50	4	US-09-293-505-6
c	864	16.6	1.1	50	4	US-09-617-871-6
c	865	16.6	1.1	50	4	US-09-354-947-495
	866	16.6	1.1	50	4	US-09-354-947-571
c	867	16.6	1.1	50	4	US-09-097-239-40
	868	16.6	1.1	50	4	US-08-880-865-9
c	869	16.6	1.1	50	5	PCT-US93-12388-495
	870	16.6	1.1	50	5	PCT-US93-12388-571
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c	872	16.4	1.0	18	4	US-09-669-974-23
	873	16.4	1.0	20	3	US-09-358-382-10
	874	16.4	1.0	26	1	US-08-487-141B-43
	875	16.4	1.0	26	2	US-08-927-561-43
	876	16.4	1.0	26	4	US-09-429-349-9
	877	16.4	1.0	26	5	PCT-US96-09388-43
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	879	16.4	1.0	27	1	US-08-758-306-204
c	880	16.4	1.0	27	2	US-08-413-806-1
	881	16.4	1.0	27	3	US-08-884-324-25
	882	16.4	1.0	27	4	US-08-584-040-5100
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	885	16.4	1.0	28	3	US-08-863-813A-38
c	886	16.4	1.0	28	4	US-08-676-318A-38
c	887	16.4	1.0	28	4	US-09-281-481A-2
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	889	16.4	1.0	30	6	5520913-28
	890	16.4	1.0	31	2	US-08-576-626A-10
	891	16.4	1.0	33	1	US-08-258-026A-9
	892	16.4	1.0	33	4	US-09-605-785-488
	893	16.4	1.0	33	4	US-09-439-313-488
	894	16.4	1.0	33	5	PCT-US95-07541-9
c	895	16.4	1.0	34	3	US-09-282-996-11
	896	16.4	1.0	35	4	US-09-708-426-6
c	897	16.4	1.0	35	5	PCT-US95-06987-3
	898	16.4	1.0	36	1	US-08-311-760A-157
	899	16.4	1.0	36	1	US-08-480-449-13
c	900	16.4	1.0	36	1	US-08-608-437-1
	901	16.4	1.0	36	1	US-08-608-437-2
c	902	16.4	1.0	36	2	US-08-452-724A-10
	903	16.4	1.0	36	2	US-08-585-684B-585

Sequence 6, Appli
Sequence 29, Appl
Sequence 933, App
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Patent No. 5520913
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Sequence 157, App
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Sequence 2, Appli
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Sequence 585, App

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	906	16.4	1.0	36	4	US-09-038-073-585
	907	16.4	1.0	36	4	US-08-479-603-13
	908	16.4	1.0	37	2	US-07-814-220-29
	909	16.4	1.0	37	2	US-07-812-421-29
	910	16.4	1.0	38	1	US-08-373-124A-685
	911	16.4	1.0	38	1	US-08-373-124A-2360
c	912	16.4	1.0	38	1	US-08-530-492-17
	913	16.4	1.0	38	1	US-08-435-628-685
	914	16.4	1.0	38	1	US-08-435-628-2360
	915	16.4	1.0	38	2	US-08-731-272A-7
c	916	16.4	1.0	38	4	US-08-906-517-17
c	917	16.4	1.0	39	2	US-08-647-449-28
	918	16.4	1.0	39	2	US-08-761-277A-62
c	919	16.4	1.0	39	4	US-09-281-792B-28
	920	16.4	1.0	40	1	US-07-949-488A-6
c	921	16.4	1.0	40	1	US-08-030-731A-25
c	922	16.4	1.0	40	4	US-09-476-256-27
c	923	16.4	1.0	41	2	US-07-814-220-28
c	924	16.4	1.0	41	2	US-07-812-421-28
c	925	16.4	1.0	41	4	US-09-402-631A-1
	926	16.4	1.0	42	1	US-08-464-136-75
	927	16.4	1.0	42	2	US-08-349-131-75
	928	16.4	1.0	42	3	US-08-470-297A-75
	929	16.4	1.0	42	4	US-09-641-638-887
	930	16.4	1.0	42	5	PCT-US91-07149-75
	931	16.4	1.0	43	1	US-08-406-635-1
	932	16.4	1.0	43	1	US-08-406-635-4
c	933	16.4	1.0	43	3	US-09-068-738A-14
c	934	16.4	1.0	43	4	US-09-162-484-15
c	935	16.4	1.0	43	4	US-09-025-769B-324
	936	16.4	1.0	43	4	US-08-672-213-66
	937	16.4	1.0	43	4	US-09-153-310-23
	938	16.4	1.0	43	4	US-09-117-860-44
c	939	16.4	1.0	43	4	US-09-117-860-46
	940	16.4	1.0	43	4	US-09-410-903-74
c	941	16.4	1.0	44	2	US-08-637-899-6
c	942	16.4	1.0	44	2	US-08-982-232-4
c	943	16.4	1.0	44	2	US-09-128-312-11
c	944	16.4	1.0	44	4	US-09-370-683-11
c	945	16.4	1.0	45	1	US-08-171-389-66
c	946	16.4	1.0	45	1	US-08-123-936-66
c	947	16.4	1.0	45	1	US-08-418-123A-1
c	948	16.4	1.0	45	2	US-08-475-228A-66
	949	16.4	1.0	45	2	US-08-982-232-16
	950	16.4	1.0	45	2	US-08-860-174A-16
c	951	16.4	1.0	45	3	US-08-482-080A-66
	952	16.4	1.0	45	4	US-09-171-025-9
c	953	16.4	1.0	45	4	US-09-354-947-66
	954	16.4	1.0	45	4	US-09-561-490E-42
c	955	16.4	1.0	45	5	PCT-US93-12388-66
c	956	16.4	1.0	46	1	US-08-484-192-180
	957	16.4	1.0	47	1	US-08-103-739B-3
	958	16.4	1.0	47	1	US-08-474-404-3
	959	16.4	1.0	47	2	US-08-790-963-54
	960	16.4	1.0	47	2	US-08-485-845-3
	961	16.4	1.0	47	2	US-08-482-714-3
	962	16.4	1.0	47	3	US-09-068-738A-13
	963	16.4	1.0	47	4	US-09-371-774-54
	964	16.4	1.0	47	4	US-09-211-416-3
	965	16.4	1.0	47	4	US-09-059-958-3
	966	16.4	1.0	47	4	US-09-641-638-848
c	967	16.4	1.0	47	4	US-09-641-638-1087
c	968	16.4	1.0	47	5	PCT-US93-08435-31
c	969	16.4	1.0	47	6	5284931-23
	970	16.4	1.0	48	1	US-07-750-080A-1
	971	16.4	1.0	48	3	US-08-338-579A-36
	972	16.4	1.0	48	3	US-08-651-472-1
	973	16.4	1.0	48	4	US-08-358-928-1
	974	16.4	1.0	48	4	US-08-957-351-32
c	975	16.4	1.0	48	4	US-09-500-123-3
	976	16.4	1.0	48	5	PCT-US94-09851-36

Sequence 157, App
Sequence 13, Appl
Sequence 585, App
Sequence 13, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 685, App
Sequence 2360, Ap
Sequence 17, Appl
Sequence 685, App
Sequence 2360, Ap
Sequence 7, Appli
Sequence 17, Appl
Sequence 28, Appl
Sequence 62, Appl
Sequence 28, Appl
Sequence 6, Appli
Sequence 25, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 1, Appli
Sequence 75, Appl
Sequence 75, Appl
Sequence 75, Appl
Sequence 887, App
Sequence 75, Appl
Sequence 1, Appli
Sequence 4, Appli
Sequence 14, Appl
Sequence 15, Appl
Sequence 324, App
Sequence 66, Appl
Sequence 23, Appl
Sequence 44, Appl
Sequence 46, Appl
Sequence 74, Appl
Sequence 6, Appli
Sequence 4, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 1, Appli
Sequence 66, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 66, Appl
Sequence 9, Appli
Sequence 66, Appl
Sequence 42, Appl
Sequence 66, Appl
Sequence 180, App
Sequence 3, Appli
Sequence 3, Appli
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Sequence 3, Appli
Sequence 13, Appl
Sequence 54, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 848, App
Sequence 1087, Ap
Sequence 31, Appl
Patent No. 5284931
Sequence 1, Appli
Sequence 36, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 32, Appl
Sequence 3, Appli
Sequence 36, Appl

977	16.4	1.0	49	1	US-08-484-493-4	Sequence 4, Appli
978	16.4	1.0	49	1	US-08-484-494-4	Sequence 4, Appli
979	16.4	1.0	49	2	US-08-345-212-4	Sequence 4, Appli
980	16.4	1.0	49	3	US-09-184-658-55	Sequence 55, Appl
981	16.4	1.0	49	3	US-09-249-003-4	Sequence 4, Appli
c 982	16.4	1.0	50	1	US-08-171-389-422	Sequence 422, App
c 983	16.4	1.0	50	1	US-08-171-389-481	Sequence 481, App
c 984	16.4	1.0	50	1	US-08-123-936-422	Sequence 422, App
c 985	16.4	1.0	50	1	US-08-123-936-481	Sequence 481, App
986	16.4	1.0	50	2	US-08-765-512-2	Sequence 2, Appli
c 987	16.4	1.0	50	2	US-08-475-228A-422	Sequence 422, App
c 988	16.4	1.0	50	2	US-08-475-228A-481	Sequence 481, App
989	16.4	1.0	50	2	US-08-914-828-2	Sequence 2, Appli
c 990	16.4	1.0	50	3	US-08-482-080A-422	Sequence 422, App
c 991	16.4	1.0	50	3	US-08-482-080A-481	Sequence 481, App
992	16.4	1.0	50	3	US-08-907-392A-2	Sequence 2, Appli
993	16.4	1.0	50	3	US-08-892-747-10	Sequence 10, Appl
994	16.4	1.0	50	3	US-08-983-607-5	Sequence 5, Appli
995	16.4	1.0	50	3	US-08-983-607-42	Sequence 42, Appl
996	16.4	1.0	50	4	US-08-849-567A-60	Sequence 60, Appl
c 997	16.4	1.0	50	4	US-09-354-947-422	Sequence 422, App
c 998	16.4	1.0	50	4	US-09-354-947-481	Sequence 481, App
c 999	16.4	1.0	50	5	PCT-US93-12388-422	Sequence 422, App
c1000	16.4	1.0	50	5	PCT-US93-12388-481	Sequence 481, App

ALIGNMENTS

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RESULT 1
US-09-325-256-31/c
; Sequence 31, Application US/09325256
; Patent No. 6444793
; GENERAL INFORMATION:
;  APPLICANT:  PEPINSKY, R. BLAKE
;  APPLICANT:  BAKER, DARREN P.
;  APPLICANT:  WEN, DINGYI
;  APPLICANT:  WILLIAMS, KEVIN P.
;  APPLICANT:  GARGER, ELLEN A.
;  APPLICANT:  TAYLOR, FREDERICK R.
;  APPLICANT:  GALDES, ALPHONSE
;  APPLICANT:  PORTER, JEFFREY
;  TITLE OF INVENTION:  HYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND
;  TITLE OF INVENTION:  METHODS
;  FILE REFERENCE:  BIV-067.01
;  CURRENT APPLICATION NUMBER: US/09/325,256
;  CURRENT FILING DATE:  1999-06-03
;  PRIOR APPLICATION NUMBER:  60/099,800
;  PRIOR FILING DATE:  1998-09-10
;  PRIOR APPLICATION NUMBER:  60/078,935
;  PRIOR FILING DATE:  1998-03-20
;  PRIOR APPLICATION NUMBER:  60/089,685
;  PRIOR FILING DATE:  1998-06-17
;  PRIOR APPLICATION NUMBER:  60/067,423
;  PRIOR FILING DATE:  1997-12-03
;  PRIOR APPLICATION NUMBER:  PCT/US98/25676
;  PRIOR FILING DATE:  1998-12-03
;  NUMBER OF SEQ ID NOS:  31
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 49
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-325-256-31

  Query Match             2.3%;  Score 36;  DB 4;  Length 49;
  Best Local Similarity   88.6%;  Pred. No. 50;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    703 GGTGAAAGCAGAGAACTCGGTGGCGGCCAAATCGGGAGGCTGCT 746
          ||||||||||||||||||||||   || ||||||||||||||| |
Db     49 GGTGAAAGCAGAGAACTCGGTGTGCGCAAAATCGGGAGGCTGAT 6


RESULT 2
US-09-930-181-14
; Sequence 14, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
;  APPLICANT: OriGene Technologies
;  TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
;  FILE REFERENCE: 16U 101 V1
;  CURRENT APPLICATION NUMBER: US/09/930,181
;  CURRENT FILING DATE:  2001-08-16
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-930-181-14

  Query Match             1.8%;  Score 28.2;  DB 4;  Length 50;
  Best Local Similarity   73.5%;  Pred. No. 1.7e+03;
  Matches   36;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy   1336 GGACCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGC 1384
          ||  || |||| || |  ||||||||| | | |||| ||||||||  ||
Db      1 GGCGCGGGGCGCGGGCCTCGGCGGCGGCGGCGGCGGCGGCGGAAGC 49


RESULT 3
US-09-580-923-35
; Sequence 35, Application US/09580923
; Patent No. 6319672
; GENERAL INFORMATION:
;  APPLICANT:  Crouzet, Joel
;  APPLICANT:  Scherman, Daniel
;  APPLICANT:  Wils, Pierre
;  APPLICANT:  Cameron, Beatrice
;  APPLICANT:  Blanche, Francis
;  TITLE OF INVENTION:  PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
;  TITLE OF INVENTION:  IMMOBILIZED OLIGONUCLEOTIDE
;  FILE REFERENCE:  03804.0138-01
;  CURRENT APPLICATION NUMBER: US/09/580,923
;  CURRENT FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  08/860,038
;  PRIOR FILING DATE:  1997-06-09
;  PRIOR APPLICATION NUMBER:  PCT/FR95/01468
;  PRIOR FILING DATE:  1995-11-08
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 35
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: oligonucleotide
US-09-580-923-35

  Query Match             1.6%;  Score 26;  DB 4;  Length 50;
  Best Local Similarity   70.0%;  Pred. No. 4.5e+03;
  Matches   35;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     19 GAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGA 68
          ||||||| ||| | | |||   ||| |||  || || || |  ||||||||
Db      1 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 50


RESULT 4
US-08-068-747-7
; Sequence 7, Application US/08068747
; Patent No. 5695933
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;  GENERAL INFORMATION:
;    APPLICANT:  Schalling, Martin
;    APPLICANT:  Hudson, Thomas J.
;    APPLICANT:  Housman, David E.
;    TITLE OF INVENTION:  Direct Determination of Expanded
;    TITLE OF INVENTION:  Nucleotide Repeats in the Human Genome
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusett
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/068,747
;      FILING DATE:  28-MAY-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  MIT-6141
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Synthetic"
US-08-068-747-7

  Query Match             1.6%;  Score 25;  DB 1;  Length 33;
  Best Local Similarity   84.8%;  Pred. No. 6.6e+03;
  Matches   28;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    1351 CAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGG 1383
           | |||||||||| | | |||| ||||||||||
Db       1 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 33


RESULT 5
US-08-846-020A-6
; Sequence 6, Application US/08846020A
; Patent No. 6090547
;  GENERAL INFORMATION:
;    APPLICANT:  Drazen M.D., Jeffrey M.
;    APPLICANT:  In M.D., Kwang-Ho
;    APPLICANT:  Asano M.D., Koichiro
;    APPLICANT:  Beier, David
;    APPLICANT:  Grobholz, James
;    TITLE OF INVENTION:  5-Lipoxygenase Gene Sequence
;    TITLE OF INVENTION:  Polymorphisms and Their Use in Classifying Patients
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHOATE, HALL & STEWART
;      STREET:  53 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2891
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/846,020A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jarrell Ph.D., Brenda H.
;      REGISTRATION NUMBER:  39,223
;      REFERENCE/DOCKET NUMBER:  0092662-0012
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-5000
;      TELEFAX:  (617) 248 4000
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  No. 6090547mal tandem SP1 binding motif with 6 base
;      CLONE:  pair deletion
US-08-846-020A-6

  Query Match             1.6%;  Score 24.6;  DB 3;  Length 50;
  Best Local Similarity   76.9%;  Pred. No. 8.3e+03;
  Matches   30;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy    1348 GGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCAG 1386
           | || |||| ||||||| | | || || ||||| |||||
Db       6 GTACTGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCAG 44


RESULT 6
US-09-617-871-6
; Sequence 6, Application US/09617871
; Patent No. 6355434
;  GENERAL INFORMATION:
;    APPLICANT:  Drazen M.D., Jeffrey M.
;    APPLICANT:  In M.D., Kwang-Ho
;    APPLICANT:  Asano M.D., Koichiro
;    APPLICANT:  Beier, David
;    APPLICANT:  Grobholz, James
;    TITLE OF INVENTION:  5-Lipoxygenase Gene Sequence
;    TITLE OF INVENTION:  Polymorphisms and Their Use in Classifying Patients
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHOATE, HALL & STEWART
;      STREET:  53 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2891
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/617,871
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/846,020
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jarrell Ph.D., Brenda H.
;      REGISTRATION NUMBER:  39,223
;      REFERENCE/DOCKET NUMBER:  0092662-0012
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-5000
;      TELEFAX:  (617) 248 4000
;  INFORMATION FOR SEQ ID NO:  6:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  No. 6355434mal tandem SP1 binding motif with 6 base
;      CLONE:  pair deletion
US-09-617-871-6

  Query Match             1.6%;  Score 24.6;  DB 4;  Length 50;
  Best Local Similarity   76.9%;  Pred. No. 8.3e+03;
  Matches   30;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   1348 GGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCAG 1386
          | || |||| ||||||| | | || || ||||| |||||
Db      6 GTACTGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGGCAG 44


RESULT 7
US-08-748-591-11
; Sequence 11, Application US/08748591
; Patent No. 5759811
;  GENERAL INFORMATION:
;    APPLICANT:  Epstein, Ervin
;    APPLICANT:  Hu, Zhilan
;    APPLICANT:  Bonifas, Jeanette
;    TITLE OF INVENTION:  Mutant Human Hedgehog Gene
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish and Richardson
;      STREET:  2200 Sand Hill Road
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/748,591
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sherwood, Pamela J
;      REGISTRATION NUMBER:  36,677
;      REFERENCE/DOCKET NUMBER:  06510/067001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 322-5070
;      TELEFAX:  (415) 854-0875
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-748-591-11

  Query Match             1.5%;  Score 24;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+03;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    524 ACCGAGGGCTGGGACGAAGATGGC 547
          ||||||||||||||||||||||||
Db      1 ACCGAGGGCTGGGACGAAGATGGC 24


RESULT 8
US-08-356-060A-43
; Sequence 43, Application US/08356060A
; Patent No. 5844079
;  GENERAL INFORMATION:
;    APPLICANT:  Ingham, Phillip W.
;    APPLICANT:  McMahon, Andrew P.
;    APPLICANT:  Tabin, Clifford J.
;    TITLE OF INVENTION:  Vertebrate Embryonic Pattern-Inducing
;    TITLE OF INVENTION:  Proteins and Uses Related Thereto
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,060A
;      FILING DATE:  14-DEC-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/176,427
;      FILING DATE:  30-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMI-006CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-356-060A-43

  Query Match             1.5%;  Score 24;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+03;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    524 ACCGAGGGCTGGGACGAAGATGGC 547
          ||||||||||||||||||||||||
Db      1 ACCGAGGGCTGGGACGAAGATGGC 24


RESULT 9
US-08-460-900C-43
; Sequence 43, Application US/08460900C
; Patent No. 6165747
;  GENERAL INFORMATION:
;    APPLICANT:  Ingham, Phillip W.
;    APPLICANT:  McMahon, Andrew P.
;    APPLICANT:  Tabin, Clifford J.
;    APPLICANT:  Bumcrot, David A.
;    APPLICANT:  Marti-Gorostiza, Elisa
;    TITLE OF INVENTION:  Vertebrate Embryonic Pattern-Inducing
;    TITLE OF INVENTION:  Proteins and Uses Related Thereto
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
```

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;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/460,900C
;       FILING DATE:  5-JUNE-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/435,093
;       FILING DATE:  4-MAY-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/356,060
;       FILING DATE:  14-DEC-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/176,427
;       FILING DATE:  30-DEC-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Vincent, Matthew P.
;       REGISTRATION NUMBER:  36,709
;       REFERENCE/DOCKET NUMBER:  HMV-006.05
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 832-1000
;       TELEFAX:  (617) 832-7000
;   INFORMATION FOR SEQ ID NO:  43:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  24 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-460-900C-43

  Query Match             1.5%;  Score 24;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+03;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     524 ACCGAGGGCTGGGACGAAGATGGC 547
           ||||||||||||||||||||||||
Db       1 ACCGAGGGCTGGGACGAAGATGGC 24


RESULT 10
US-08-674-509B-43
; Sequence 43, Application US/08674509B
; Patent No. 6261786
;  GENERAL INFORMATION:
;    APPLICANT:  Ingham, Phillip W.
;    APPLICANT:  McMahon, Andrew P.
;    APPLICANT:  Tabin, Clifford J.
;    APPLICANT:  Marigo, Valeria
;    TITLE OF INVENTION:  SCREENING ASSAYS FOR HEDGEGOG AGONISTS
;    TITLE OF INVENTION:  AND ANTAGONISTS
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/674,509B
;      FILING DATE:  02-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/460,900
;      FILING DATE:  05-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMV-006.06
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "primer"
US-08-674-509B-43

  Query Match             1.5%;  Score 24;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+03;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     524 ACCGAGGGCTGGGACGAAGATGGC 547
           ||||||||||||||||||||||||
Db       1 ACCGAGGGCTGGGACGAAGATGGC 24


RESULT 11
US-08-954-698-43
; Sequence 43, Application US/08954698
; Patent No. 6271363
;  GENERAL INFORMATION:
;    APPLICANT:  Ingham, Phillip W.
;    APPLICANT:  McMahon, Andrew P.
;    APPLICANT:  Tabin, Clifford J.
;    TITLE OF INVENTION:  Vertebrate Embryonic Pattern-Inducing
;    TITLE OF INVENTION:  Proteins and Uses Related Thereto
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/954,698
;      FILING DATE:  20-OCT-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/462,386
;      FILING DATE:  05-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/435,093
;      FILING DATE:  04-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/356,060
;      FILING DATE:  14-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/176,427
;      FILING DATE:  30-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMV-006.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-954-698-43

  Query Match             1.5%;  Score 24;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+03;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     524 ACCGAGGGCTGGGACGAAGATGGC 547
           ||||||||||||||||||||||||
Db       1 ACCGAGGGCTGGGACGAAGATGGC 24


RESULT 12
US-08-957-874-43
; Sequence 43, Application US/08957874
; Patent No. 6384192
;  GENERAL INFORMATION:
;    APPLICANT:  Ingham, Phillip W.
;    APPLICANT:  McMahon, Andrew P.
;    APPLICANT:  Tabin, Clifford J.
;    TITLE OF INVENTION:  Vertebrate Embryonic Pattern-Inducing
;    TITLE OF INVENTION:  Proteins and Uses Related Thereto
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/957,874
;      FILING DATE:  20-OCT-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/462,386
;      FILING DATE:  5-JUNE-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/435,093
;      FILING DATE:  4-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/356,060
;      FILING DATE:  14-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/176,427
;      FILING DATE:  30-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMV-006.09
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 832-1000
;      TELEFAX:  (617) 832-7000
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-957-874-43

  Query Match             1.5%;  Score 24;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+03;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     524 ACCGAGGGCTGGGACGAAGATGGC 547
           ||||||||||||||||||||||||
Db       1 ACCGAGGGCTGGGACGAAGATGGC 24


RESULT 13
US-08-258-026A-13
; Sequence 13, Application US/08258026A
; Patent No. 5516637
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Grace P.
;    APPLICANT:  Rhode, Peter R.
;    APPLICANT:  Stinson, Jeffrey R.
;    APPLICANT:  Wong, Hing C.
;    TITLE OF INVENTION:  A METHOD FOR DISPLAYING PROTEINS
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David G. Conlin; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/258,026A
;      FILING DATE:  10-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resnick, David R.
;      REGISTRATION NUMBER:  34235
;      REFERENCE/DOCKET NUMBER:  42838
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 523-3400
;      TELEFAX:  (617) 523-6400
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
US-08-258-026A-13

  Query Match             1.5%;  Score 24;  DB 1;  Length 45;
  Best Local Similarity   75.0%;  Pred. No. 1.1e+04;
  Matches   30;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    1341 GCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGG 1380
           | ||||| | ||||||||| || |    ||| ||||||||
Db       2 GTGGCGGTGGCAGCGGCGGTGGTGGTTCCGGAGGCGGCGG 41


RESULT 14
US-09-813-781-129
; Sequence 129, Application US/09813781
; Patent No. 6405989
; GENERAL INFORMATION:
;  APPLICANT: WEIDANZ, JON A.
;  APPLICANT:  CARD, KIMBERLYN F.
;  APPLICANT:  WONG, HING C.
;  TITLE OF INVENTION: FUSION PROTEINS COMPRISING BACTERIOPHAGE COAT PROTEIN
;  TITLE OF INVENTION:  AND A SINGLE-CHAIN T-CELL RECEPTOR
;  FILE REFERENCE: 46745(1758)
;  CURRENT APPLICATION NUMBER: US/09/813,781
;  CURRENT FILING DATE:  2001-03-22
;  NUMBER OF SEQ ID NOS: 130
```

```
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
;   LENGTH: 45
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-813-781-129

  Query Match             1.5%;  Score 24;  DB 4;  Length 45;
  Best Local Similarity   75.0%;  Pred. No. 1.1e+04;
  Matches   30;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy   1341 GCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGG 1380
          | ||||| | ||||||||| || |    ||| ||||||||
Db      2 GTGGCGGTGGCAGCGGCGGTGGTGGTTCCGGAGGCGGCGG 41


RESULT 15
PCT-US95-07541-13
; Sequence 13, Application PC/TUS9507541
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Grace P.
;    APPLICANT:  Rhode, Peter R.
;    APPLICANT:  Stinson, Jeffrey R.
;    APPLICANT:  Wong, Hing C.
;    TITLE OF INVENTION:  A METHOD FOR DISPLAYING
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David G. Conlin; DIKE, BRONSTEIN,
;      ADDRESSEE:  ROBERTS & CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/07541
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/258,026
;      FILING DATE:  10-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resnick, David R.
;      REGISTRATION NUMBER:  34235
;      REFERENCE/DOCKET NUMBER:  42838
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 523-3400
;      TELEFAX:  (617) 523-6400
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
PCT-US95-07541-13

  Query Match             1.5%;  Score 24;  DB 5;  Length 45;
  Best Local Similarity   75.0%;  Pred. No. 1.1e+04;
  Matches   30;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy   1341 GCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGG 1380
          | ||||| | ||||||||| || |    ||| ||||||||
Db      2 GTGGCGGTGGCAGCGGCGGTGGTGGTTCCGGAGGCGGCGG 41


RESULT 16
US-08-068-747-2/c
; Sequence 2, Application US/08068747
; Patent No. 5695933
;  GENERAL INFORMATION:
;    APPLICANT:  Schalling, Martin
;    APPLICANT:  Hudson, Thomas J.
;    APPLICANT:  Housman, David E.
;    TITLE OF INVENTION:  Direct Determination of Expanded
;    TITLE OF INVENTION:  Nucleotide Repeats in the Human Genome
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusett
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/068,747
;      FILING DATE:  28-MAY-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  MIT-6141
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Synthetic"
US-08-068-747-2

  Query Match             1.5%;  Score 23.6;  DB 1;  Length 30;
  Best Local Similarity   86.7%;  Pred. No. 1.2e+04;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1354 CGGCGGCGGGGACCGCGGGGGCGGCGGCGG 1383
          ||||||||| | | |||| ||||||||||||
Db     30 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1


RESULT 17
US-09-499-884-12
; Sequence 12, Application US/09499884
; Patent No. 6265172
; GENERAL INFORMATION:
;  APPLICANT:  St. Clair, Daret
;  APPLICANT:  Urano, Muneyasu
;  APPLICANT:  Kasarskis, Edward
;  TITLE OF INVENTION:  DIAGNOSTIC TEST AND THERAPY FOR MANGANESE SUPEROXIDE DISMU
;  TITLE OF INVENTION:  ASSOCIATED DISEASES
;  FILE REFERENCE:  50229-180
;  CURRENT APPLICATION NUMBER: US/09/499,884
;  CURRENT FILING DATE:  2000-02-08
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 38
;   TYPE: DNA
```

```
;   ORGANISM: Homo sapiens
US-09-499-884-12

  Query Match             1.5%;  Score 23.6;  DB 4;  Length 38;
  Best Local Similarity   76.3%;  Pred. No. 1.3e+04;
  Matches   29;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   1340 CGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGG 1377
          || ||||||| | |||| || ||||  || || |||||
Db      1 CGGGGCGGGGCCCGCGGGGGGGGGGGGCGGGGCGGCGG 38


RESULT 18
US-09-497-933A-19
; Sequence 19, Application US/09497933A
; Patent No. 6329147
; GENERAL INFORMATION:
;  APPLICANT:  Wagner, Robert Jr. E.
;  TITLE OF INVENTION:  METHODS FOR DETECTION OF A TRIPLET REPEAT BLOCK AND A
;  TITLE OF INVENTION:  FUNCTIONAL MISMATCH BINDING PROTEIN IN A BIOLOGICAL
;  TITLE OF INVENTION:  FLUID SAMPLE
;  FILE REFERENCE:  9408-044
;  CURRENT APPLICATION NUMBER: US/09/497,933A
;  CURRENT FILING DATE:  2000-02-04
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 48
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Probe
;   NAME/KEY: modified_base
;   LOCATION: (1)..(9)
;   OTHER INFORMATION: n = a, c, g or t
;   NAME/KEY: modified_base
;   LOCATION: (40)..(48)
;   OTHER INFORMATION: n = a, c, g or t
US-09-497-933A-19

  Query Match             1.5%;  Score 23.6;  DB 4;  Length 48;
  Best Local Similarity   86.7%;  Pred. No. 1.3e+04;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   1354 CGGCGGCGGGGACCGCGGGGGCGGCGGCGG 1383
          ||||||||| | | |||| ||||||||||||
Db     10 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 39


RESULT 19
US-09-930-181-13
; Sequence 13, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
;  APPLICANT: OriGene Technologies
;  TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
;  FILE REFERENCE: 16U 101 V1
;  CURRENT APPLICATION NUMBER: US/09/930,181
;  CURRENT FILING DATE:  2001-08-16
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-930-181-13

  Query Match             1.5%;  Score 23.6;  DB 4;  Length 50;
  Best Local Similarity   69.6%;  Pred. No. 1.3e+04;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy   1328 GCGCGCACGGACCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGG 1373
          | ||||  ||  || |||| || |  |||||||||| | | |||| |

Db      5 GGGCGCGGGGCGCGGGGCGCGGGCCTCGGCGGCGGCGGCGGCGGCG 50


RESULT 20
US-08-748-591-12/c
; Sequence 12, Application US/08748591
; Patent No. 5759811
;  GENERAL INFORMATION:
;    APPLICANT:  Epstein, Ervin
;    APPLICANT:  Hu, Zhilan
;    APPLICANT:  Bonifas, Jeanette
;    TITLE OF INVENTION:  Mutant Human Hedgehog Gene
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish and Richardson
;      STREET:  2200 Sand Hill Road
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/748,591
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sherwood, Pamela J
;      REGISTRATION NUMBER:  36,677
;      REFERENCE/DOCKET NUMBER:  06510/067001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 322-5070
;      TELEFAX:  (415) 854-0875
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-748-591-12

  Query Match             1.5%;  Score 23.4;  DB 1;  Length 25;
  Best Local Similarity   96.0%;  Pred. No. 1.3e+04;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    616 CAGCAAGTACGGCATGCTGGCCCGC 640
          ||||||||||||||||||||||| |||
Db     25 CAGCAAGTACGGCATGCTGGCTCGC 1


RESULT 21
US-09-083-123-5/c
; Sequence 5, Application US/09083123
; Patent No. 6326143
; GENERAL INFORMATION:
;  APPLICANT: Orum, Hendrik
;  APPLICANT: Seeger, Corina
;  TITLE OF INVENTION: Method for Generating Multiple Double Stranded Nucleic
;  TITLE OF INVENTION: Acids
;  FILE REFERENCE: sequence listing
;  CURRENT APPLICATION NUMBER: US/09/083,123
;  CURRENT FILING DATE: 1998-05-22
;  EARLIER APPLICATION NUMBER: EP 95118600.6
;  EARLIER FILING DATE: 1995-11-25
;  EARLIER APPLICATION NUMBER: PCT/EP96/05149
;  EARLIER FILING DATE: 1996-11-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
```

```
;   LENGTH: 32
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: made by humans
US-09-083-123-5

  Query Match             1.4%;  Score 22.4;  DB 4;  Length 32;
  Best Local Similarity   81.2%;  Pred. No. 2.1e+04;
  Matches   26;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   1543 CCGGGGGGCCGGGGGAGGGGCGCGGGAGGGGG 1574
          ||||||||  ||||| |||| | ||| |||||
Db     32 CCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1


RESULT 22
US-09-325-256-30
; Sequence 30, Application US/09325256
; Patent No. 6444793
; GENERAL INFORMATION:
;  APPLICANT:  PEPINSKY, R. BLAKE
;  APPLICANT:  BAKER, DARREN P.
;  APPLICANT:  WEN, DINGYI
;  APPLICANT:  WILLIAMS, KEVIN P.
;  APPLICANT:  GARGER, ELLEN A.
;  APPLICANT:  TAYLOR, FREDERICK R.
;  APPLICANT:  GALDES, ALPHONSE
;  APPLICANT:  PORTER, JEFFREY
;  TITLE OF INVENTION:  HYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND
;  TITLE OF INVENTION:  METHODS
;  FILE REFERENCE:  BIV-067.01
;  CURRENT APPLICATION NUMBER: US/09/325,256
;  CURRENT FILING DATE:  1999-06-03
;  PRIOR APPLICATION NUMBER:  60/099,800
;  PRIOR FILING DATE:  1998-09-10
;  PRIOR APPLICATION NUMBER:  60/078,935
;  PRIOR FILING DATE:  1998-03-20
;  PRIOR APPLICATION NUMBER:  60/089,685
;  PRIOR FILING DATE:  1998-06-17
;  PRIOR APPLICATION NUMBER:  60/067,423
;  PRIOR FILING DATE:  1997-12-03
;  PRIOR APPLICATION NUMBER:  PCT/US98/25676
;  PRIOR FILING DATE:  1998-12-03
;  NUMBER OF SEQ ID NOS:  31
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-325-256-30

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  Best Local Similarity   100.0%;  Pred. No. 2.7e+04;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 23
US-08-340-045-7
; Sequence 7, Application US/08340045
; Patent No. 5637495
;  GENERAL INFORMATION:
;    APPLICANT:  AVIV, HAIM
;    APPLICANT:  GORECKI, MARIAN
;    APPLICANT:  LEVANON, AVIGDOR
;    APPLICANT:  OPPENHEIM, AMOS
;    APPLICANT:  VOGEL, TIKVA
;    APPLICANT:  ZEELON, ELISHA
;    APPLICANT:  ZEEVI, MENACHEM
;    TITLE OF INVENTION:  PLASMIDS FOR PRODUCTION OF HUMAN GROWTH
;    TITLE OF INVENTION:  HORMONE OR POLYPEPTIDE ANALOG THEREOF, HOSTS CONTAINING
;    TITLE OF INVENTION:  THE PLASMIDS, PRODUCTS MANUFACTURED THEREBY, AND RELATED
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  COOPER & DUNHAM LLP
;      STREET:  1185 AVENUE OF THE AMERICAS
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/340,045
;      FILING DATE:  14-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WHITE, JOHN P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  20065-G/JPW/GJG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0525
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-340-045-7

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  Best Local Similarity   78.8%;  Pred. No. 2.8e+04;
  Matches   26;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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RESULT 24
US-08-871-302A-7
; Sequence 7, Application US/08871302A
; Patent No. 6054291
;  GENERAL INFORMATION:
;    APPLICANT:  AVIV, HAIM
;    APPLICANT:  GORECKI, MARIAN
;    APPLICANT:  LEVANON, AVIGDOR
;    APPLICANT:  OPPENHEIM, AMOS
;    APPLICANT:  VOGEL, TIKVA
;    APPLICANT:  ZEELON, ELISHA
;    APPLICANT:  ZEEVI, MENACHEM
;    TITLE OF INVENTION:  PLASMIDS FOR PRODUCTION OF HUMAN GROWTH
;    TITLE OF INVENTION:  HORMONE OR POLYPEPTIDE ANALOG THEREOF, HOSTS CONTAINING
;    TITLE OF INVENTION:  THE PLASMIDS, PRODUCTS MANUFACTURED THEREBY, AND RELATED
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  COOPER & DUNHAM LLP
;      STREET:  1185 AVENUE OF THE AMERICAS
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
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;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/871,302A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/340,045
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WHITE, JOHN P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  20065-G/JPW/GJG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0525
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-871-302A-7

  Query Match             1.4%;  Score 21.8;  DB 3;  Length 35;
  Best Local Similarity   78.8%;  Pred. No. 2.8e+04;
  Matches   26;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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RESULT 25
US-09-485-737B-5
; Sequence 5, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
;  APPLICANT: Buyse, Marie-Ange
;  APPLICANT:  Sablon, Erwin
;  TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
;  TITLE OF INVENTION:  CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
;  FILE REFERENCE: INNS:015
;  CURRENT APPLICATION NUMBER: US/09/485,737B
;  CURRENT FILING DATE:  2000-02-14
;  PRIOR APPLICATION NUMBER: PCT/EP 98/05165
;  PRIOR FILING DATE: 1998-08-14
;  PRIOR APPLICATION NUMBER: EPO 98870139.7
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: EPO 97870122.5
;  PRIOR FILING DATE: 1997-08-18
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 40
;   TYPE: DNA
;   ORGANISM: UNKNOWN
;   FEATURE:
;   OTHER INFORMATION: GENOMIC
US-09-485-737B-5

  Query Match             1.4%;  Score 21.6;  DB 4;  Length 40;
  Best Local Similarity   75.0%;  Pred. No. 3.1e+04;
  Matches   27;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

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GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-001-844-3
Perfect score: 1576
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 501302 seqs, 350932545 residues

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Post-processing: Minimum Match 0%
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Listing first 1000 summaries

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	3	22	1.4	30	10	US-09-828-034-7	Sequence 7, Appli
	4	21.4	1.4	45	9	US-10-006-856A-151	Sequence 151, App
	5	20.8	1.3	45	9	US-10-135-984-6	Sequence 6, Appli
	6	20.8	1.3	46	9	US-10-135-984-4	Sequence 4, Appli
c	7	20.8	1.3	46	9	US-10-135-984-5	Sequence 5, Appli
c	8	20.8	1.3	46	9	US-10-135-984-7	Sequence 7, Appli
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	12	20.2	1.3	48	12	US-10-072-152-32	Sequence 32, Appl
	13	20	1.3	45	9	US-09-992-598-122	Sequence 122, App
	14	20	1.3	45	9	US-09-989-293A-122	Sequence 122, App
	15	20	1.3	45	9	US-09-989-735-122	Sequence 122, App
	16	20	1.3	45	9	US-09-990-444-122	Sequence 122, App
	17	20	1.3	45	9	US-09-989-730-122	Sequence 122, App
	18	20	1.3	45	9	US-09-990-436-122	Sequence 122, App
	19	20	1.3	45	9	US-09-991-181-122	Sequence 122, App
	20	20	1.3	45	9	US-09-993-687-122	Sequence 122, App
	21	20	1.3	45	9	US-09-989-734-122	Sequence 122, App
	22	20	1.3	45	9	US-09-997-653-122	Sequence 122, App
	23	20	1.3	45	9	US-09-993-667-122	Sequence 122, App
	24	20	1.3	45	9	US-10-211-069-35	Sequence 35, Appl
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	28	20	1.3	45	9	US-09-997-666-122	Sequence 122, App
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	33	20	1.3	45	10	US-09-989-722-122	Sequence 122, App
	34	20	1.3	45	10	US-09-989-723-122	Sequence 122, App
	35	20	1.3	45	10	US-09-989-279-122	Sequence 122, App
	36	20	1.3	45	10	US-09-989-727-122	Sequence 122, App
	37	20	1.3	45	10	US-09-989-731-122	Sequence 122, App
	38	20	1.3	45	10	US-09-989-732-122	Sequence 122, App
	39	20	1.3	45	10	US-09-991-073-122	Sequence 122, App
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	43	20	1.3	45	10	US-09-990-456-122	Sequence 122, App
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	47	19.4	1.2	50	9	US-09-765-555-25	Sequence 25, Appl
	48	19.2	1.2	36	9	US-09-997-868-28	Sequence 28, Appl
	49	19	1.2	30	9	US-09-883-848A-36	Sequence 36, Appl
	50	19	1.2	36	9	US-09-966-781A-15	Sequence 15, Appl
c	51	19	1.2	41	9	US-09-749-873-105	Sequence 105, App
	52	19	1.2	47	10	US-09-785-632A-7	Sequence 7, Appli
c	53	19	1.2	50	10	US-09-782-650-16	Sequence 16, Appl
	54	18.8	1.2	40	9	US-09-876-082-75	Sequence 75, Appl
	55	18.8	1.2	40	9	US-09-875-082-75	Sequence 75, Appl
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	59	18.8	1.2	50	10	US-09-874-547-6	Sequence 6, Appli
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	75	18.6	1.2	45	9	US-09-906-742-313	Sequence 313, App
c	76	18.6	1.2	45	9	US-09-993-667-122	Sequence 122, App
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c	110	18.6	1.2	45	10	US-09-989-721-122	Sequence 122, App
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	122	18.4	1.2	45	10	US-09-944-449-53	Sequence 53, Appl
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	125	18.4	1.2	45	10	US-09-945-015-53	Sequence 53, Appl
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	127	18.4	1.2	45	10	US-09-944-097-53	Sequence 53, Appl
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	140	18.2	1.2	45	10	US-09-893-615-71	Sequence 71, Appl
	141	18	1.1	35	9	US-09-735-056-4	Sequence 4, Appli
	142	18	1.1	42	10	US-09-845-160-12	Sequence 12, Appl
	143	18	1.1	43	10	US-09-894-788-20	Sequence 20, Appl
	144	18	1.1	43	10	US-09-894-796-20	Sequence 20, Appl
	145	17.8	1.1	31	9	US-09-912-263-430	Sequence 430, App
	146	17.8	1.1	31	10	US-09-801-274-125	Sequence 125, App
	147	17.8	1.1	31	10	US-09-801-274-1526	Sequence 1526, Ap
	148	17.8	1.1	39	9	US-10-067-790-45	Sequence 45, Appl
	149	17.8	1.1	39	9	US-10-067-892-45	Sequence 45, Appl
	150	17.8	1.1	39	9	US-09-539-382-45	Sequence 45, Appl
	151	17.8	1.1	39	9	US-10-067-893-45	Sequence 45, Appl
c	152	17.8	1.1	39	10	US-09-760-574-57	Sequence 57, Appl
	153	17.6	1.1	30	10	US-09-892-074-7	Sequence 7, Appli
c	154	17.6	1.1	32	10	US-09-896-650A-20	Sequence 20, Appl
c	155	17.6	1.1	40	9	US-09-826-025-19	Sequence 19, Appl
c	156	17.6	1.1	41	9	US-09-733-042-23	Sequence 23, Appl
c	157	17.6	1.1	41	10	US-09-875-519A-1	Sequence 1, Appli
c	158	17.6	1.1	42	9	US-10-083-590-7	Sequence 7, Appli
	159	17.6	1.1	44	7	US-08-325-278-7	Sequence 7, Appli
	160	17.6	1.1	47	9	US-09-853-526-269	Sequence 269, App
c	161	17.6	1.1	47	10	US-09-912-165-7	Sequence 7, Appli
	162	17.6	1.1	47	10	US-09-901-484A-269	Sequence 269, App
	163	17.6	1.1	48	9	US-09-978-917A-29	Sequence 29, Appl
c	164	17.6	1.1	48	9	US-09-978-917A-30	Sequence 30, Appl
	165	17.6	1.1	50	9	US-10-125-751-17	Sequence 17, Appl
	166	17.6	1.1	50	9	US-09-912-552-17	Sequence 17, Appl
	167	17.6	1.1	50	9	US-10-036-949-39	Sequence 39, Appl
	168	17.6	1.1	50	10	US-09-740-002-7	Sequence 7, Appli
	169	17.6	1.1	50	10	US-09-918-029-17	Sequence 17, Appl
	170	17.6	1.1	50	12	US-10-038-271-17	Sequence 17, Appl
c	171	17.4	1.1	31	9	US-09-912-263-496	Sequence 496, App
c	172	17.4	1.1	31	10	US-09-801-274-213	Sequence 213, App
c	173	17.4	1.1	31	10	US-09-801-274-219	Sequence 219, App
	174	17.4	1.1	31	10	US-09-801-274-676	Sequence 676, App
	175	17.4	1.1	31	10	US-09-801-274-959	Sequence 959, App
	176	17.4	1.1	31	10	US-09-801-274-1211	Sequence 1211, Ap
	177	17.4	1.1	35	9	US-09-771-009-70	Sequence 70, Appl
	178	17.4	1.1	35	10	US-09-732-348-8	Sequence 8, Appli
c	179	17.4	1.1	45	9	US-10-007-132-7	Sequence 7, Appli
c	180	17.4	1.1	49	10	US-09-785-632A-8	Sequence 8, Appli
	181	17.4	1.1	50	8	US-08-978-633-28	Sequence 28, Appl
c	182	17.4	1.1	50	8	US-08-978-633-29	Sequence 29, Appl
	183	17.4	1.1	50	8	US-08-978-634-28	Sequence 28, Appl
c	184	17.4	1.1	50	8	US-08-978-634-29	Sequence 29, Appl
	185	17.4	1.1	50	8	US-08-978-637-28	Sequence 28, Appl
c	186	17.4	1.1	50	8	US-08-978-637-29	Sequence 29, Appl
	187	17.4	1.1	50	8	US-08-978-632-28	Sequence 28, Appl
c	188	17.4	1.1	50	8	US-08-978-632-29	Sequence 29, Appl
	189	17.4	1.1	50	9	US-10-073-300-14	Sequence 14, Appl
	190	17.4	1.1	50	9	US-10-073-300-15	Sequence 15, Appl
c	191	17.4	1.1	50	9	US-09-765-555-23	Sequence 23, Appl
c	192	17.2	1.1	24	9	US-09-837-621-31	Sequence 31, Appl
c	193	17.2	1.1	24	10	US-09-788-038-31	Sequence 31, Appl
c	194	17.2	1.1	30	9	US-09-953-052-21	Sequence 21, Appl
	195	17.2	1.1	31	9	US-09-912-263-286	Sequence 286, App
c	196	17.2	1.1	42	9	US-09-252-150-41	Sequence 41, Appl
c	197	17.2	1.1	42	10	US-09-845-160-13	Sequence 13, Appl
	198	17.2	1.1	48	10	US-09-971-798-25	Sequence 25, Appl
	199	17.2	1.1	49	10	US-09-740-002-8	Sequence 8, Appli
c	200	17.2	1.1	50	9	US-09-765-555-25	Sequence 25, Appl
	201	17.2	1.1	50	10	US-09-874-547-5	Sequence 5, Appli
	202	17.2	1.1	50	10	US-09-874-547-9	Sequence 9, Appli
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	205	17	1.1	32	10	US-09-828-447-31	Sequence 31, Appl
c	206	17	1.1	32	10	US-09-910-120-50	Sequence 50, Appl
c	207	17	1.1	33	9	US-10-027-961A-15	Sequence 15, Appl
c	208	17	1.1	33	9	US-09-227-718-7	Sequence 7, Appli
	209	17	1.1	35	9	US-09-991-470-7	Sequence 7, Appli
c	210	17	1.1	35	10	US-09-776-490-65	Sequence 65, Appl
c	211	17	1.1	35	10	US-09-776-491-65	Sequence 65, Appl
c	212	17	1.1	35	10	US-09-783-580-12	Sequence 12, Appl
	213	17	1.1	36	9	US-09-957-995A-24	Sequence 24, Appl
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c	215	17	1.1	37	9	US-10-096-723-8	Sequence 8, Appli
c	216	17	1.1	37	9	US-10-146-329-2	Sequence 2, Appli
c	217	17	1.1	37	10	US-09-887-854-8	Sequence 8, Appli
	218	17	1.1	39	9	US-10-067-790-49	Sequence 49, Appl
	219	17	1.1	39	9	US-10-067-892-49	Sequence 49, Appl
	220	17	1.1	39	9	US-09-539-382-49	Sequence 49, Appl
	221	17	1.1	39	9	US-10-067-893-49	Sequence 49, Appl
	222	17	1.1	39	10	US-09-874-547-26	Sequence 26, Appl
	223	17	1.1	39	10	US-09-874-547-29	Sequence 29, Appl
	224	17	1.1	40	10	US-09-245-802-128	Sequence 128, App
	225	17	1.1	42	9	US-10-225-322-12	Sequence 12, Appl
	226	17	1.1	42	10	US-09-388-089B-14	Sequence 14, Appl
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c	228	17	1.1	45	9	US-10-012-896-784	Sequence 784, App
c	229	17	1.1	45	9	US-10-135-984-6	Sequence 6, Appli
c	230	17	1.1	45	9	US-09-895-793-784	Sequence 784, App
c	231	17	1.1	45	9	US-09-895-814-784	Sequence 784, App
c	232	17	1.1	45	10	US-09-759-143-784	Sequence 784, App
c	233	17	1.1	45	10	US-09-780-669-784	Sequence 784, App
c	234	17	1.1	45	10	US-09-822-827-784	Sequence 784, App
	235	17	1.1	45	10	US-09-850-165-24	Sequence 24, Appl
	236	17	1.1	47	10	US-09-785-632A-15	Sequence 15, Appl
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	238	17	1.1	49	10	US-09-740-002-10	Sequence 10, Appl

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	241	16.8	1.1	30	9	US-10-057-467-13
	242	16.8	1.1	31	10	US-09-801-274-531
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c	245	16.8	1.1	36	10	US-09-245-487B-25
c	246	16.8	1.1	40	9	US-09-747-419-26
	247	16.8	1.1	40	9	US-09-943-722-126
	248	16.8	1.1	41	9	US-09-966-277-19
c	249	16.8	1.1	41	9	US-09-966-277-20
	250	16.8	1.1	41	9	US-09-966-930-19
c	251	16.8	1.1	41	9	US-09-966-930-20
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c	256	16.8	1.1	43	9	US-09-978-192A-450
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c	258	16.8	1.1	43	9	US-09-978-189-450
c	259	16.8	1.1	43	9	US-09-978-608A-450
	260	16.8	1.1	45	9	US-10-124-880-56
	261	16.8	1.1	48	9	US-09-864-785-3343
c	262	16.8	1.1	48	10	US-09-880-732-55
c	263	16.8	1.1	49	10	US-09-179-536B-119
c	264	16.8	1.1	50	9	US-10-012-896-969
c	265	16.8	1.1	50	9	US-09-895-814-969
c	266	16.8	1.1	50	9	US-09-765-555-29
	267	16.8	1.1	50	10	US-09-990-080-17
	268	16.6	1.1	25	10	US-09-866-108-3140
	269	16.6	1.1	25	10	US-09-866-108-3141
	270	16.6	1.1	25	10	US-09-866-108-3142
	271	16.6	1.1	31	10	US-09-911-935A-8
c	272	16.6	1.1	32	10	US-09-896-650A-18
	273	16.6	1.1	33	9	US-09-756-854-13
	274	16.6	1.1	33	9	US-10-041-574-13
c	275	16.6	1.1	33	10	US-09-757-824-1
c	276	16.6	1.1	34	9	US-10-158-895-46
c	277	16.6	1.1	36	9	US-10-057-558-35
c	278	16.6	1.1	36	9	US-10-072-438-14
c	279	16.6	1.1	36	9	US-10-072-438-28
c	280	16.6	1.1	36	9	US-10-137-765-18
c	281	16.6	1.1	36	9	US-10-146-337-18
	282	16.6	1.1	37	10	US-09-736-969A-68
	283	16.6	1.1	38	9	US-09-864-785-917
	284	16.6	1.1	38	9	US-09-864-785-1037
	285	16.6	1.1	39	9	US-10-046-922-74
	286	16.6	1.1	39	9	US-09-777-597A-12
	287	16.6	1.1	42	9	US-10-188-947-7
c	288	16.6	1.1	42	9	US-10-083-590-2
c	289	16.6	1.1	42	10	US-09-790-417-235
c	290	16.6	1.1	43	9	US-10-085-853-28
	291	16.6	1.1	45	9	US-09-735-056-22
	292	16.6	1.1	46	10	US-09-795-006A-29
c	293	16.6	1.1	48	9	US-09-995-847-22
	294	16.6	1.1	48	10	US-09-939-484-24
	295	16.6	1.1	48	10	US-09-939-483-24
	296	16.6	1.1	49	10	US-09-973-322-20
	297	16.6	1.1	50	9	US-09-990-046-6
	298	16.6	1.1	50	9	US-09-900-425A-32
c	299	16.6	1.1	50	9	US-10-125-751-18
c	300	16.6	1.1	50	9	US-09-912-552-18
c	301	16.6	1.1	50	9	US-10-011-931-12
c	302	16.6	1.1	50	9	US-10-036-949-40
	303	16.6	1.1	50	9	US-10-079-185-32
c	304	16.6	1.1	50	10	US-09-912-436-15
c	305	16.6	1.1	50	10	US-09-918-029-18
c	306	16.6	1.1	50	10	US-09-900-062-44
c	307	16.6	1.1	50	12	US-10-038-271-18
c	308	16.4	1.0	18	10	US-09-797-862-23
	309	16.4	1.0	21	10	US-09-798-058-13
c	310	16.4	1.0	27	10	US-09-735-363A-6
	311	16.4	1.0	28	10	US-09-867-475-4

Sequence 9, Appli
Sequence 17, Appl
Sequence 13, Appl
Sequence 531, App
Sequence 1526, Ap
Sequence 8, Appli
Sequence 25, Appl
Sequence 26, Appl
Sequence 126, App
Sequence 19, Appl
Sequence 20, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 5, Appli
Sequence 450, App
Sequence 12, Appl
Sequence 450, App
Sequence 450, App
Sequence 450, App
Sequence 450, App
Sequence 450, App
Sequence 56, Appl
Sequence 3343, Ap
Sequence 55, Appl
Sequence 119, App
Sequence 969, App
Sequence 969, App
Sequence 29, Appl
Sequence 17, Appl
Sequence 3140, Ap
Sequence 3141, Ap
Sequence 3142, Ap
Sequence 8, Appli
Sequence 18, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 1, Appli
Sequence 46, Appl
Sequence 35, Appl
Sequence 14, Appl
Sequence 28, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 68, Appl
Sequence 917, App
Sequence 1037, Ap
Sequence 74, Appl
Sequence 12, Appl
Sequence 7, Appli
Sequence 2, Appli
Sequence 235, App
Sequence 28, Appl
Sequence 22, Appl
Sequence 29, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 20, Appl
Sequence 6, Appli
Sequence 32, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 12, Appl
Sequence 40, Appl
Sequence 32, Appl
Sequence 15, Appl
Sequence 18, Appl
Sequence 44, Appl
Sequence 18, Appl
Sequence 23, Appl
Sequence 13, Appl
Sequence 6, Appli
Sequence 4, Appli

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	313	16.4	1.0	30	9	US-09-841-236C-3
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	315	16.4	1.0	31	10	US-09-801-274-740
	316	16.4	1.0	31	10	US-09-801-274-825
c	317	16.4	1.0	31	10	US-09-801-274-1737
	318	16.4	1.0	31	10	US-09-777-430A-16
	319	16.4	1.0	32	10	US-09-480-236-11
	320	16.4	1.0	33	9	US-10-012-896-488
	321	16.4	1.0	33	9	US-09-895-793-488
	322	16.4	1.0	33	9	US-09-895-814-488
	323	16.4	1.0	33	10	US-09-759-143-488
	324	16.4	1.0	33	10	US-09-780-669-488
	325	16.4	1.0	33	10	US-09-822-827-488
	326	16.4	1.0	33	10	US-09-971-798-15
	327	16.4	1.0	35	9	US-09-988-115A-68
	328	16.4	1.0	36	9	US-09-733-042-24
	329	16.4	1.0	36	10	US-09-504-231A-1701
	330	16.4	1.0	36	10	US-09-504-231A-2479
	331	16.4	1.0	36	10	US-09-245-487B-27
	332	16.4	1.0	36	10	US-09-274-553D-1701
	333	16.4	1.0	36	10	US-09-274-553D-2479
	334	16.4	1.0	39	9	US-09-925-664-62
	335	16.4	1.0	39	10	US-09-874-547-28
c	336	16.4	1.0	40	9	US-10-125-635A-371
	337	16.4	1.0	40	10	US-09-814-292-16
	338	16.4	1.0	42	9	US-10-097-597-11
	339	16.4	1.0	42	9	US-10-097-580-11
c	340	16.4	1.0	42	9	US-10-045-631A-23
	341	16.4	1.0	42	10	US-09-445-023A-11
c	342	16.4	1.0	45	9	US-09-957-641-10
	343	16.4	1.0	45	9	US-09-957-641-18
	344	16.4	1.0	45	9	US-10-211-069-42
	345	16.4	1.0	45	10	US-09-742-693-3
	346	16.4	1.0	45	10	US-09-893-615-68
	347	16.4	1.0	45	10	US-09-893-615-72
	348	16.4	1.0	47	9	US-09-876-082-54
	349	16.4	1.0	47	9	US-09-875-082-54
	350	16.4	1.0	48	9	US-09-991-209-8
c	351	16.4	1.0	48	9	US-10-090-215-3
	352	16.4	1.0	49	10	US-09-785-632A-9
	353	16.4	1.0	50	10	US-09-874-547-11
c	354	16.2	1.0	21	10	US-09-828-034-10
	355	16.2	1.0	22	9	US-09-837-621-32
c	356	16.2	1.0	22	9	US-09-837-621-35
	357	16.2	1.0	22	10	US-09-788-038-32
c	358	16.2	1.0	22	10	US-09-788-038-35
c	359	16.2	1.0	24	9	US-09-837-621-28
c	360	16.2	1.0	24	9	US-09-837-621-29
c	361	16.2	1.0	24	9	US-09-837-621-30
c	362	16.2	1.0	24	10	US-09-788-038-28
c	363	16.2	1.0	24	10	US-09-788-038-29
c	364	16.2	1.0	24	10	US-09-788-038-30
	365	16.2	1.0	25	10	US-09-866-108-3143
	366	16.2	1.0	25	10	US-09-866-108-3144
c	367	16.2	1.0	27	10	US-09-965-553-39
	368	16.2	1.0	29	10	US-09-899-917-7
	369	16.2	1.0	29	10	US-09-899-917-10
	370	16.2	1.0	30	9	US-09-953-052-5
c	371	16.2	1.0	30	9	US-09-953-052-7
	372	16.2	1.0	30	10	US-09-897-042-10
	373	16.2	1.0	31	9	US-09-961-077-414
	374	16.2	1.0	31	9	US-09-912-263-39
	375	16.2	1.0	31	9	US-09-912-263-212
	376	16.2	1.0	31	9	US-09-912-263-243
c	377	16.2	1.0	31	9	US-09-912-263-371
	378	16.2	1.0	31	10	US-09-801-274-181
	379	16.2	1.0	31	10	US-09-801-274-337
	380	16.2	1.0	31	10	US-09-801-274-1345
c	381	16.2	1.0	31	10	US-09-801-274-1423
	382	16.2	1.0	31	10	US-09-801-274-1594
	383	16.2	1.0	31	10	US-09-801-274-1601
	384	16.2	1.0	32	9	US-09-847-101B-41

Sequence 4, Appli
Sequence 3, Appli
Sequence 162, App
Sequence 740, App
Sequence 825, App
Sequence 1737, Ap
Sequence 16, Appl
Sequence 11, Appl
Sequence 488, App
Sequence 488, App
Sequence 488, App
Sequence 488, App
Sequence 488, App
Sequence 488, App
Sequence 15, Appl
Sequence 68, Appl
Sequence 24, Appl
Sequence 1701, Ap
Sequence 2479, Ap
Sequence 27, Appl
Sequence 1701, Ap
Sequence 2479, Ap
Sequence 62, Appl
Sequence 28, Appl
Sequence 371, App
Sequence 16, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 23, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 18, Appl
Sequence 42, Appl
Sequence 3, Appli
Sequence 68, Appl
Sequence 72, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 8, Appli
Sequence 3, Appli
Sequence 9, Appli
Sequence 11, Appl
Sequence 10, Appl
Sequence 32, Appl
Sequence 35, Appl
Sequence 32, Appl
Sequence 35, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 3143, Ap
Sequence 3144, Ap
Sequence 39, Appl
Sequence 7, Appli
Sequence 10, Appl
Sequence 5, Appli
Sequence 7, Appli
Sequence 10, Appl
Sequence 414, App
Sequence 39, Appl
Sequence 212, App
Sequence 243, App
Sequence 371, App
Sequence 181, App
Sequence 337, App
Sequence 1345, Ap
Sequence 1423, Ap
Sequence 1594, Ap
Sequence 1601, Ap
Sequence 41, Appl

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c	386	16.2	1.0	35	9	US-09-850-514-48
	387	16.2	1.0	36	9	US-09-991-209-62
	388	16.2	1.0	37	10	US-09-504-231A-3220
	389	16.2	1.0	37	10	US-09-760-574-13
	390	16.2	1.0	38	9	US-09-864-785-780
	391	16.2	1.0	38	9	US-10-201-310-6
	392	16.2	1.0	38	9	US-09-941-492-30
	393	16.2	1.0	38	10	US-09-874-547-62
	394	16.2	1.0	38	10	US-09-874-547-76
	395	16.2	1.0	38	10	US-09-756-095-30
c	396	16.2	1.0	39	9	US-09-925-664-4
	397	16.2	1.0	39	9	US-09-925-664-5
c	398	16.2	1.0	41	9	US-09-998-425-52
c	399	16.2	1.0	41	9	US-09-997-977-52
	400	16.2	1.0	42	9	US-09-862-393-2
c	401	16.2	1.0	42	9	US-10-038-723-74
	402	16.2	1.0	42	10	US-09-727-311-48
c	403	16.2	1.0	42	10	US-09-790-417-233
c	404	16.2	1.0	42	10	US-09-843-856-7
c	405	16.2	1.0	42	10	US-09-765-111A-9
	406	16.2	1.0	43	9	US-09-905-291A-173
	407	16.2	1.0	43	9	US-09-902-853-173
	408	16.2	1.0	43	9	US-09-907-824-173
	409	16.2	1.0	43	9	US-09-907-841-173
	410	16.2	1.0	43	9	US-09-904-011-173
	411	16.2	1.0	43	9	US-09-906-742-173
	412	16.2	1.0	43	9	US-09-906-838-173
	413	16.2	1.0	43	9	US-09-907-613-173
	414	16.2	1.0	43	9	US-09-907-942-173
	415	16.2	1.0	43	9	US-09-904-820-173
	416	16.2	1.0	43	9	US-09-904-859-173
	417	16.2	1.0	43	9	US-09-909-204-173
	418	16.2	1.0	43	9	US-09-904-786-173
	419	16.2	1.0	43	9	US-09-906-646-173
	420	16.2	1.0	43	9	US-09-906-700-173
	421	16.2	1.0	43	9	US-09-902-903-173
	422	16.2	1.0	43	9	US-09-903-749A-173
	423	16.2	1.0	43	9	US-09-903-786-173
	424	16.2	1.0	43	10	US-09-909-320-173
	425	16.2	1.0	43	10	US-09-909-088B-173
	426	16.2	1.0	45	9	US-10-125-751-22
	427	16.2	1.0	45	9	US-10-036-949-47
c	428	16.2	1.0	45	10	US-09-735-995-96
	429	16.2	1.0	45	10	US-09-976-787-18
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	431	16.2	1.0	45	10	US-09-865-198-18
	432	16.2	1.0	45	10	US-09-900-062-47
	433	16.2	1.0	45	12	US-10-038-271-22
c	434	16.2	1.0	46	10	US-09-758-386-14
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	437	16.2	1.0	47	9	US-10-121-746-61
	438	16.2	1.0	47	10	US-09-740-002-3
	439	16.2	1.0	48	9	US-09-943-722-39
c	440	16.2	1.0	48	10	US-09-971-798-25
c	441	16.2	1.0	50	9	US-10-011-931-28
	442	16.2	1.0	50	9	US-09-765-555-23
	443	16.2	1.0	50	10	US-09-920-171-38
c	444	16.2	1.0	50	10	US-09-946-175-43
c	445	16	1.0	24	9	US-09-888-326-170
	446	16	1.0	25	9	US-09-872-462-442
	447	16	1.0	25	9	US-09-872-462-443
c	448	16	1.0	25	10	US-09-866-108-4465
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c	451	16	1.0	25	10	US-09-866-108-4886
c	452	16	1.0	25	10	US-09-896-650A-26
	453	16	1.0	29	10	US-09-729-674-242
c	454	16	1.0	29	10	US-09-993-170-55
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Sequence 234, App
Sequence 48, Appl
Sequence 62, Appl
Sequence 3220, Ap
Sequence 13, Appl
Sequence 780, App
Sequence 6, Appli
Sequence 30, Appl
Sequence 62, Appl
Sequence 76, Appl
Sequence 30, Appl
Sequence 4, Appli
Sequence 5, Appli
Sequence 52, Appl
Sequence 52, Appl
Sequence 2, Appli
Sequence 74, Appl
Sequence 48, Appl
Sequence 233, App
Sequence 7, Appli
Sequence 9, Appli
Sequence 173, App
Sequence 173, App
Sequence 173, App
Sequence 173, App
Sequence 173, App
Sequence 173, App
Sequence 173, App
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Sequence 173, App
Sequence 173, App
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Sequence 173, App
Sequence 173, App
Sequence 173, App
Sequence 173, App
Sequence 173, App
Sequence 173, App
Sequence 22, Appl
Sequence 47, Appl
Sequence 96, Appl
Sequence 18, Appl
Sequence 22, Appl
Sequence 18, Appl
Sequence 47, Appl
Sequence 22, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 8, Appli
Sequence 61, Appl
Sequence 3, Appli
Sequence 39, Appl
Sequence 25, Appl
Sequence 28, Appl
Sequence 23, Appl
Sequence 38, Appl
Sequence 43, Appl
Sequence 170, App
Sequence 442, App
Sequence 443, App
Sequence 4465, Ap
Sequence 4466, Ap
Sequence 4885, Ap
Sequence 4886, Ap
Sequence 26, Appl
Sequence 242, App
Sequence 55, Appl
Sequence 21, Appl
Sequence 787, App
Sequence 882, App

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	466	16	1.0	37	10	US-09-788-209A-3
	467	16	1.0	38	9	US-09-864-785-821
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	469	16	1.0	38	9	US-09-864-785-1097
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c	471	16	1.0	39	9	US-09-996-140-22
	472	16	1.0	39	9	US-09-925-664-60
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	483	16	1.0	43	9	US-09-376-940-23
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	485	16	1.0	43	10	US-09-766-898-12
	486	16	1.0	43	10	US-09-766-916-12
c	487	16	1.0	44	9	US-09-252-150-48
	488	16	1.0	44	9	US-09-996-634-159
c	489	16	1.0	45	9	US-09-905-291A-37
c	490	16	1.0	45	9	US-09-902-853-37
c	491	16	1.0	45	9	US-09-907-824-37
c	492	16	1.0	45	9	US-09-907-841-37
c	493	16	1.0	45	9	US-09-904-011-37
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	510	16	1.0	46	10	US-09-788-209A-16
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	513	16	1.0	47	9	US-09-853-526-250
c	514	16	1.0	47	9	US-10-211-069-27
c	515	16	1.0	47	10	US-09-785-632A-14
	516	16	1.0	47	10	US-09-901-484A-192
	517	16	1.0	47	10	US-09-901-484A-250
	518	16	1.0	49	9	US-09-796-679-15
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	520	16	1.0	49	10	US-09-920-552-125
	521	16	1.0	50	9	US-10-007-132-8
c	522	16	1.0	50	10	US-09-284-663A-30
	523	16	1.0	50	10	US-09-874-547-12
	524	16	1.0	50	10	US-09-783-590-12183
	525	16	1.0	50	10	US-09-223-490-20
	526	15.8	1.0	20	9	US-09-888-326-410
c	527	15.8	1.0	20	10	US-09-791-406-46
	528	15.8	1.0	21	10	US-09-984-183-22
	529	15.8	1.0	24	10	US-09-766-378A-31
c	530	15.8	1.0	25	10	US-09-771-838A-13

Sequence 989, App
Sequence 62, Appl
Sequence 4, Appli
Sequence 21, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 21, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 821, App
Sequence 874, App
Sequence 1097, Ap
Sequence 1212, Ap
Sequence 22, Appl
Sequence 60, Appl
Sequence 23, Appl
Sequence 15, Appl
Sequence 11, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 4, Appli
Sequence 99, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 48, Appl
Sequence 159, App
Sequence 37, Appl
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Sequence 37, Appl
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Sequence 37, Appl
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Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 5, Appli
Sequence 192, App
Sequence 250, App
Sequence 27, Appl
Sequence 14, Appl
Sequence 192, App
Sequence 250, App
Sequence 15, Appl
Sequence 25, Appl
Sequence 125, App
Sequence 8, Appli
Sequence 30, Appl
Sequence 12, Appl
Sequence 12183, A
Sequence 20, Appl
Sequence 410, App
Sequence 46, Appl
Sequence 22, Appl
Sequence 31, Appl
Sequence 13, Appl

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c	535	15.8	1.0	25	10	US-09-866-108-10887 Sequence 10887, A
c	536	15.8	1.0	25	10	US-09-866-108-10888 Sequence 10888, A
c	537	15.8	1.0	25	10	US-09-866-108-10889 Sequence 10889, A
c	538	15.8	1.0	27	9	US-10-041-090-2 Sequence 2, Appli
c	539	15.8	1.0	27	9	US-09-877-705A-61 Sequence 61, Appl
	540	15.8	1.0	27	9	US-09-877-705A-62 Sequence 62, Appl
c	541	15.8	1.0	27	9	US-09-877-738A-61 Sequence 61, Appl
	542	15.8	1.0	27	9	US-09-877-738A-62 Sequence 62, Appl
	543	15.8	1.0	27	10	US-09-735-363A-3 Sequence 3, Appli
	544	15.8	1.0	27	10	US-09-735-363A-68 Sequence 68, Appl
c	545	15.8	1.0	27	10	US-09-894-633A-41 Sequence 41, Appl
	546	15.8	1.0	27	12	US-10-017-828-14 Sequence 14, Appl
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c	555	15.8	1.0	28	10	US-09-944-457-9 Sequence 9, Appli
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c	557	15.8	1.0	28	10	US-09-945-015-9 Sequence 9, Appli
c	558	15.8	1.0	28	10	US-09-944-396-9 Sequence 9, Appli
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	565	15.8	1.0	30	9	US-09-953-052-16 Sequence 16, Appl
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	567	15.8	1.0	30	10	US-09-292-973-18 Sequence 18, Appl
	568	15.8	1.0	30	10	US-09-965-099-27 Sequence 27, Appl
	569	15.8	1.0	30	12	US-10-051-852-27 Sequence 27, Appl
	570	15.8	1.0	31	9	US-09-778-900A-12 Sequence 12, Appl
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c	575	15.8	1.0	33	9	US-09-932-367A-62 Sequence 62, Appl
	576	15.8	1.0	34	9	US-10-124-880-58 Sequence 58, Appl
	577	15.8	1.0	34	10	US-09-790-417-232 Sequence 232, App
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c	579	15.8	1.0	36	9	US-09-907-111-219 Sequence 219, App
c	580	15.8	1.0	36	9	US-10-056-414-402 Sequence 402, App
c	581	15.8	1.0	37	9	US-10-192-085-9 Sequence 9, Appli
	582	15.8	1.0	37	10	US-09-847-185-49 Sequence 49, Appl
	583	15.8	1.0	38	9	US-09-864-785-1108 Sequence 1108, Ap
c	584	15.8	1.0	38	9	US-09-864-785-1398 Sequence 1398, Ap
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c	586	15.8	1.0	39	9	US-09-211-424-27 Sequence 27, Appl
	587	15.8	1.0	39	9	US-10-079-818-31 Sequence 31, Appl
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c	589	15.8	1.0	39	12	US-10-139-262-32 Sequence 32, Appl
c	590	15.8	1.0	40	9	US-10-101-392-16 Sequence 16, Appl
c	591	15.8	1.0	40	9	US-10-101-392-18 Sequence 18, Appl
	592	15.8	1.0	41	9	US-10-119-466-10 Sequence 10, Appl
c	593	15.8	1.0	41	9	US-09-185-904A-27 Sequence 27, Appl
	594	15.8	1.0	41	9	US-09-988-462-87 Sequence 87, Appl
c	595	15.8	1.0	41	10	US-09-811-094-27 Sequence 27, Appl
c	596	15.8	1.0	41	10	US-09-810-644-27 Sequence 27, Appl
	597	15.8	1.0	44	9	US-09-950-335A-15 Sequence 15, Appl
	598	15.8	1.0	45	9	US-09-905-291A-94 Sequence 94, Appl
c	599	15.8	1.0	45	9	US-09-925-664-73 Sequence 73, Appl
c	600	15.8	1.0	45	9	US-09-925-922-15 Sequence 15, Appl
	601	15.8	1.0	45	9	US-09-902-853-94 Sequence 94, Appl
	602	15.8	1.0	45	9	US-09-907-824-94 Sequence 94, Appl
	603	15.8	1.0	45	9	US-09-907-841-94 Sequence 94, Appl
	604	15.8	1.0	45	9	US-09-904-011-94 Sequence 94, Appl
	605	15.8	1.0	45	9	US-09-906-742-94 Sequence 94, Appl
c	606	15.8	1.0	45	9	US-10-211-069-33 Sequence 33, Appl
	607	15.8	1.0	45	9	US-09-906-838-94 Sequence 94, Appl
	608	15.8	1.0	45	9	US-09-907-613-94 Sequence 94, Appl
	609	15.8	1.0	45	9	US-09-907-942-94 Sequence 94, Appl
	610	15.8	1.0	45	9	US-09-904-820-94 Sequence 94, Appl
	611	15.8	1.0	45	9	US-09-904-859-94 Sequence 94, Appl
	612	15.8	1.0	45	9	US-09-909-204-94 Sequence 94, Appl
	613	15.8	1.0	45	9	US-09-904-786-94 Sequence 94, Appl
	614	15.8	1.0	45	9	US-09-906-646-94 Sequence 94, Appl
	615	15.8	1.0	45	9	US-09-906-700-94 Sequence 94, Appl
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	618	15.8	1.0	45	9	US-09-903-786-94 Sequence 94, Appl
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	620	15.8	1.0	45	10	US-09-909-320-94 Sequence 94, Appl
	621	15.8	1.0	45	10	US-09-772-719-17 Sequence 17, Appl
	622	15.8	1.0	45	10	US-09-896-650A-1 Sequence 1, Appli
	623	15.8	1.0	45	10	US-09-909-088B-94 Sequence 94, Appl
	624	15.8	1.0	46	9	US-09-900-379-64 Sequence 64, Appl
	625	15.8	1.0	46	10	US-09-216-393-362 Sequence 362, App
	626	15.8	1.0	46	10	US-09-766-898-14 Sequence 14, Appl
	627	15.8	1.0	46	10	US-09-766-898-25 Sequence 25, Appl
	628	15.8	1.0	46	10	US-09-766-916-14 Sequence 14, Appl
	629	15.8	1.0	46	10	US-09-766-916-25 Sequence 25, Appl
	630	15.8	1.0	46	10	US-09-848-164-64 Sequence 64, Appl
	631	15.8	1.0	46	10	US-09-384-472-5 Sequence 5, Appli
	632	15.8	1.0	47	10	US-09-785-632A-13 Sequence 13, Appl
	633	15.8	1.0	47	10	US-09-880-732-56 Sequence 56, Appl
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c	635	15.8	1.0	50	9	US-10-103-002-12 Sequence 12, Appl
c	636	15.8	1.0	50	9	US-10-103-002-13 Sequence 13, Appl
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	638	15.8	1.0	50	10	US-09-227-913-1 Sequence 1, Appli
c	639	15.8	1.0	50	10	US-09-227-913-3 Sequence 3, Appli
	640	15.8	1.0	50	10	US-09-896-650A-29 Sequence 29, Appl
	641	15.6	1.0	25	9	US-09-872-462-440 Sequence 440, App
	642	15.6	1.0	25	9	US-09-872-462-441 Sequence 441, App
	643	15.6	1.0	25	10	US-09-866-108-3139 Sequence 3139, Ap
c	644	15.6	1.0	25	10	US-09-866-108-4467 Sequence 4467, Ap
c	645	15.6	1.0	25	10	US-09-866-108-4468 Sequence 4468, Ap
	646	15.6	1.0	25	10	US-09-801-042-3 Sequence 3, Appli
c	647	15.6	1.0	26	8	US-08-900-220C-26 Sequence 26, Appl
c	648	15.6	1.0	26	10	US-09-815-171A-31 Sequence 31, Appl
c	649	15.6	1.0	26	10	US-09-151-999-26 Sequence 26, Appl
c	650	15.6	1.0	27	7	US-08-834-705-55 Sequence 55, Appl
c	651	15.6	1.0	27	9	US-10-135-984-3 Sequence 3, Appli
	652	15.6	1.0	27	10	US-09-870-956-38 Sequence 38, Appl
	653	15.6	1.0	29	9	US-10-135-984-2 Sequence 2, Appli
c	654	15.6	1.0	30	9	US-09-976-736-27 Sequence 27, Appl
c	655	15.6	1.0	30	9	US-09-953-052-9 Sequence 9, Appli
	656	15.6	1.0	30	9	US-10-113-877-155 Sequence 155, App
	657	15.6	1.0	30	10	US-09-420-433-79 Sequence 79, Appl
	658	15.6	1.0	31	9	US-09-288-971-5 Sequence 5, Appli
c	659	15.6	1.0	31	9	US-09-288-971-9 Sequence 9, Appli
	660	15.6	1.0	31	9	US-09-288-971-13 Sequence 13, Appl
c	661	15.6	1.0	31	9	US-09-288-971-15 Sequence 15, Appl
c	662	15.6	1.0	31	9	US-09-912-263-3 Sequence 3, Appli
	663	15.6	1.0	31	9	US-09-912-263-502 Sequence 502, App
	664	15.6	1.0	31	10	US-09-801-274-158 Sequence 158, App
	665	15.6	1.0	31	10	US-09-801-274-1362 Sequence 1362, Ap
c	666	15.6	1.0	31	10	US-09-801-274-1414 Sequence 1414, Ap
	667	15.6	1.0	31	10	US-09-801-274-1471 Sequence 1471, Ap
c	668	15.6	1.0	31	10	US-09-896-650A-22 Sequence 22, Appl
	669	15.6	1.0	33	9	US-09-991-209-57 Sequence 57, Appl
	670	15.6	1.0	33	9	US-09-991-209-67 Sequence 67, Appl
	671	15.6	1.0	33	10	US-09-840-762A-7 Sequence 7, Appli
	672	15.6	1.0	33	10	US-09-983-531A-34 Sequence 34, Appl
c	673	15.6	1.0	34	9	US-10-012-896-901 Sequence 901, App
c	674	15.6	1.0	34	9	US-09-778-900A-24 Sequence 24, Appl
c	675	15.6	1.0	34	9	US-09-895-793-901 Sequence 901, App
c	676	15.6	1.0	34	9	US-09-895-814-901 Sequence 901, App

c 677	15.6	1.0	34	10	US-09-759-143-901	Sequence 901, App
c 678	15.6	1.0	34	10	US-09-780-669-901	Sequence 901, App
c 679	15.6	1.0	34	10	US-09-822-827-901	Sequence 901, App
c 680	15.6	1.0	35	9	US-09-861-257-100	Sequence 100, App
c 681	15.6	1.0	35	10	US-09-735-705-384	Sequence 384, App
c 682	15.6	1.0	35	10	US-09-850-716A-384	Sequence 384, App
c 683	15.6	1.0	35	10	US-09-897-778-384	Sequence 384, App
c 684	15.6	1.0	36	9	US-09-991-209-62	Sequence 62, Appl
685	15.6	1.0	36	10	US-09-873-676-68	Sequence 68, Appl
686	15.6	1.0	36	10	US-09-974-248-5	Sequence 5, Appli
687	15.6	1.0	37	10	US-09-250-611-105	Sequence 105, App
688	15.6	1.0	38	9	US-10-028-410-4	Sequence 4, Appli
c 689	15.6	1.0	38	9	US-09-825-805-1157	Sequence 1157, Ap
690	15.6	1.0	38	9	US-10-125-635A-370	Sequence 370, App
691	15.6	1.0	38	10	US-09-874-547-69	Sequence 69, Appl
692	15.6	1.0	38	10	US-09-876-527-18	Sequence 18, Appl
c 693	15.6	1.0	39	10	US-09-758-386-4	Sequence 4, Appli
694	15.6	1.0	39	10	US-09-784-990-25	Sequence 25, Appl
695	15.6	1.0	39	10	US-09-179-536B-247	Sequence 247, App
696	15.6	1.0	39	10	US-09-854-799-6	Sequence 6, Appli
697	15.6	1.0	39	10	US-09-469-522-14	Sequence 14, Appl
c 698	15.6	1.0	40	9	US-10-158-684-1	Sequence 1, Appli
c 699	15.6	1.0	40	9	US-10-158-711-1	Sequence 1, Appli
700	15.6	1.0	40	10	US-09-179-536B-248	Sequence 248, App
701	15.6	1.0	40	10	US-09-931-184-6	Sequence 6, Appli
c 702	15.6	1.0	41	10	US-09-238-351-29	Sequence 29, Appl
c 703	15.6	1.0	41	10	US-09-238-351-40	Sequence 40, Appl
704	15.6	1.0	41	10	US-09-179-536B-249	Sequence 249, App
c 705	15.6	1.0	41	10	US-09-858-994-12	Sequence 12, Appl
c 706	15.6	1.0	42	9	US-09-185-904A-29	Sequence 29, Appl
c 707	15.6	1.0	42	9	US-09-887-784-11	Sequence 11, Appl
708	15.6	1.0	42	9	US-09-887-784-12	Sequence 12, Appl
c 709	15.6	1.0	42	10	US-09-811-094-29	Sequence 29, Appl
c 710	15.6	1.0	42	10	US-09-811-094-35	Sequence 35, Appl
c 711	15.6	1.0	42	10	US-09-810-644-29	Sequence 29, Appl
c 712	15.6	1.0	42	10	US-09-810-644-35	Sequence 35, Appl
713	15.6	1.0	42	10	US-09-179-536B-250	Sequence 250, App
c 714	15.6	1.0	43	9	US-09-792-630-48	Sequence 48, Appl
715	15.6	1.0	43	9	US-09-944-160-17	Sequence 17, Appl
c 716	15.6	1.0	43	9	US-10-080-376-48	Sequence 48, Appl
717	15.6	1.0	43	9	US-10-033-297-97	Sequence 97, Appl
c 718	15.6	1.0	43	9	US-09-991-209-80	Sequence 80, Appl
c 719	15.6	1.0	43	9	US-09-953-351-48	Sequence 48, Appl
720	15.6	1.0	43	9	US-09-940-244-97	Sequence 97, Appl
721	15.6	1.0	43	10	US-09-179-536B-251	Sequence 251, App
c 722	15.6	1.0	43	10	US-09-027-287-40	Sequence 40, Appl
c 723	15.6	1.0	43	10	US-09-252-656B-40	Sequence 40, Appl
724	15.6	1.0	44	9	US-09-905-291A-21	Sequence 21, Appl
c 725	15.6	1.0	44	9	US-09-908-153B-9	Sequence 9, Appli
726	15.6	1.0	44	9	US-09-902-853-21	Sequence 21, Appl
727	15.6	1.0	44	9	US-09-907-824-21	Sequence 21, Appl
728	15.6	1.0	44	9	US-09-907-841-21	Sequence 21, Appl
729	15.6	1.0	44	9	US-09-904-011-21	Sequence 21, Appl
730	15.6	1.0	44	9	US-09-749-873-106	Sequence 106, App
731	15.6	1.0	44	9	US-09-906-742-21	Sequence 21, Appl
732	15.6	1.0	44	9	US-09-906-838-21	Sequence 21, Appl
733	15.6	1.0	44	9	US-09-907-613-21	Sequence 21, Appl
734	15.6	1.0	44	9	US-09-907-942-21	Sequence 21, Appl
735	15.6	1.0	44	9	US-09-904-820-21	Sequence 21, Appl
736	15.6	1.0	44	9	US-09-904-859-21	Sequence 21, Appl
737	15.6	1.0	44	9	US-09-909-204-21	Sequence 21, Appl
738	15.6	1.0	44	9	US-09-904-786-21	Sequence 21, Appl
739	15.6	1.0	44	9	US-09-906-646-21	Sequence 21, Appl
740	15.6	1.0	44	9	US-09-906-700-21	Sequence 21, Appl
741	15.6	1.0	44	9	US-09-902-903-21	Sequence 21, Appl
742	15.6	1.0	44	9	US-09-903-749A-21	Sequence 21, Appl
743	15.6	1.0	44	9	US-09-903-786-21	Sequence 21, Appl
744	15.6	1.0	44	10	US-09-179-536B-252	Sequence 252, App
745	15.6	1.0	44	10	US-09-909-320-21	Sequence 21, Appl
746	15.6	1.0	44	10	US-09-909-088B-21	Sequence 21, Appl
c 747	15.6	1.0	45	9	US-09-990-046-22	Sequence 22, Appl
748	15.6	1.0	45	9	US-09-925-922-7	Sequence 7, Appli
749	15.6	1.0	45	9	US-09-293-854-20	Sequence 20, Appl
c 750	15.6	1.0	45	9	US-10-125-751-22	Sequence 22, Appl
c 751	15.6	1.0	45	9	US-10-036-949-47	Sequence 47, Appl
752	15.6	1.0	45	10	US-09-179-536B-253	Sequence 253, App
753	15.6	1.0	45	10	US-09-808-037-10	Sequence 10, Appl
754	15.6	1.0	45	10	US-09-740-668A-72	Sequence 72, Appl
755	15.6	1.0	45	10	US-09-893-615-69	Sequence 69, Appl
c 756	15.6	1.0	45	10	US-09-918-029-22	Sequence 22, Appl
c 757	15.6	1.0	45	10	US-09-900-062-47	Sequence 47, Appl
758	15.6	1.0	45	10	US-09-795-006A-18	Sequence 18, Appl
c 759	15.6	1.0	45	10	US-09-795-006A-38	Sequence 38, Appl
c 760	15.6	1.0	45	12	US-10-038-271-22	Sequence 22, Appl
761	15.6	1.0	46	9	US-09-978-295A-621	Sequence 621, App
762	15.6	1.0	46	9	US-09-978-697-621	Sequence 621, App
763	15.6	1.0	46	9	US-09-978-192A-621	Sequence 621, App
764	15.6	1.0	46	9	US-09-999-832A-621	Sequence 621, App
765	15.6	1.0	46	9	US-09-900-379-67	Sequence 67, Appl
c 766	15.6	1.0	46	9	US-09-900-379-68	Sequence 68, Appl
767	15.6	1.0	46	9	US-09-978-189-621	Sequence 621, App
768	15.6	1.0	46	9	US-09-991-262-14	Sequence 14, Appl
769	15.6	1.0	46	9	US-09-978-608A-621	Sequence 621, App
770	15.6	1.0	46	10	US-09-848-164-67	Sequence 67, Appl
c 771	15.6	1.0	46	10	US-09-848-164-68	Sequence 68, Appl
772	15.6	1.0	46	10	US-09-179-536B-254	Sequence 254, App
773	15.6	1.0	47	9	US-09-978-295A-378	Sequence 378, App
c 774	15.6	1.0	47	9	US-09-853-526-248	Sequence 248, App
775	15.6	1.0	47	9	US-09-978-697-378	Sequence 378, App
776	15.6	1.0	47	9	US-09-978-192A-378	Sequence 378, App
777	15.6	1.0	47	9	US-09-999-832A-378	Sequence 378, App
778	15.6	1.0	47	9	US-09-978-189-378	Sequence 378, App
779	15.6	1.0	47	9	US-09-735-056-24	Sequence 24, Appl
780	15.6	1.0	47	9	US-09-978-608A-378	Sequence 378, App
781	15.6	1.0	47	10	US-09-179-536B-255	Sequence 255, App
782	15.6	1.0	47	10	US-09-785-632A-12	Sequence 12, Appl
c 783	15.6	1.0	47	10	US-09-785-632A-12	Sequence 12, Appl
c 784	15.6	1.0	47	10	US-09-901-484A-248	Sequence 248, App
c 785	15.6	1.0	48	9	US-10-054-444-6	Sequence 6, Appli
786	15.6	1.0	48	9	US-09-864-785-3002	Sequence 3002, Ap
787	15.6	1.0	48	9	US-09-864-785-3224	Sequence 3224, Ap
788	15.6	1.0	48	10	US-09-179-536B-256	Sequence 256, App
789	15.6	1.0	48	10	US-09-880-732-55	Sequence 55, Appl
790	15.6	1.0	49	9	US-09-938-901-13	Sequence 13, Appl
791	15.6	1.0	49	10	US-09-179-536B-257	Sequence 257, App
c 792	15.6	1.0	50	9	US-10-125-751-17	Sequence 17, Appl
793	15.6	1.0	50	9	US-10-066-500-20	Sequence 20, Appl
c 794	15.6	1.0	50	9	US-09-912-552-17	Sequence 17, Appl
c 795	15.6	1.0	50	9	US-10-036-949-39	Sequence 39, Appl
796	15.6	1.0	50	9	US-10-002-796-20	Sequence 20, Appl
797	15.6	1.0	50	9	US-10-066-273-20	Sequence 20, Appl
798	15.6	1.0	50	9	US-10-066-494-20	Sequence 20, Appl
799	15.6	1.0	50	9	US-10-066-269-20	Sequence 20, Appl
800	15.6	1.0	50	9	US-10-066-193-20	Sequence 20, Appl
801	15.6	1.0	50	9	US-10-066-211-20	Sequence 20, Appl
802	15.6	1.0	50	10	US-09-179-536B-258	Sequence 258, App
c 803	15.6	1.0	50	10	US-09-920-171-38	Sequence 38, Appl
c 804	15.6	1.0	50	10	US-09-918-029-17	Sequence 17, Appl
c 805	15.6	1.0	50	10	US-09-920-300A-1257	Sequence 1257, Ap
806	15.6	1.0	50	10	US-09-739-707-7	Sequence 7, Appli
c 807	15.6	1.0	50	12	US-10-033-528-1257	Sequence 1257, Ap
c 808	15.6	1.0	50	12	US-10-038-271-17	Sequence 17, Appl
c 809	15.4	1.0	24	10	US-09-924-256A-4	Sequence 4, Appli
810	15.4	1.0	25	9	US-09-875-440-16	Sequence 16, Appl
c 811	15.4	1.0	25	9	US-09-745-317-57	Sequence 57, Appl
812	15.4	1.0	25	9	US-10-060-756A-2535	Sequence 2535, Ap
813	15.4	1.0	25	9	US-10-060-756A-3039	Sequence 3039, Ap
814	15.4	1.0	25	10	US-09-753-436-12	Sequence 12, Appl
c 815	15.4	1.0	25	10	US-09-866-108-4883	Sequence 4883, Ap
c 816	15.4	1.0	25	10	US-09-866-108-4884	Sequence 4884, Ap
c 817	15.4	1.0	25	10	US-09-866-108-11962	Sequence 11962, A
c 818	15.4	1.0	25	10	US-09-971-118-5	Sequence 5, Appli
c 819	15.4	1.0	25	10	US-09-895-040A-133	Sequence 133, App
c 820	15.4	1.0	25	10	US-09-895-040A-134	Sequence 134, App
c 821	15.4	1.0	25	10	US-09-895-040A-137	Sequence 137, App
822	15.4	1.0	26	9	US-09-988-462-92	Sequence 92, Appl

c 823	15.4	1.0	26	10	US-09-962-318-18	Sequence 18, Appl
824	15.4	1.0	26	10	US-09-263-959-538	Sequence 538, App
825	15.4	1.0	27	9	US-09-808-880-10	Sequence 10, Appl
c 826	15.4	1.0	27	10	US-09-817-014-170	Sequence 170, App
827	15.4	1.0	28	9	US-10-102-704-11	Sequence 11, Appl
828	15.4	1.0	28	9	US-10-057-951-11	Sequence 11, Appl
829	15.4	1.0	28	10	US-09-084-491A-11	Sequence 11, Appl
c 830	15.4	1.0	29	10	US-09-873-737A-13	Sequence 13, Appl
831	15.4	1.0	31	9	US-09-773-599-15	Sequence 15, Appl
c 832	15.4	1.0	31	9	US-10-023-610-103	Sequence 103, App
c 833	15.4	1.0	31	9	US-09-912-263-154	Sequence 154, App
c 834	15.4	1.0	31	9	US-09-912-263-444	Sequence 444, App
c 835	15.4	1.0	31	9	US-09-779-152-103	Sequence 103, App
836	15.4	1.0	31	10	US-09-817-360-17	Sequence 17, Appl
c 837	15.4	1.0	31	10	US-09-801-274-909	Sequence 909, App
838	15.4	1.0	31	10	US-09-801-274-928	Sequence 928, App
c 839	15.4	1.0	31	10	US-09-801-274-1085	Sequence 1085, Ap
c 840	15.4	1.0	32	10	US-09-910-120-47	Sequence 47, Appl
c 841	15.4	1.0	32	10	US-09-910-120-48	Sequence 48, Appl
c 842	15.4	1.0	32	10	US-09-910-120-52	Sequence 52, Appl
843	15.4	1.0	34	9	US-09-778-900A-24	Sequence 24, Appl
844	15.4	1.0	35	9	US-09-880-464-12	Sequence 12, Appl
845	15.4	1.0	36	9	US-09-738-444A-31	Sequence 31, Appl
846	15.4	1.0	36	10	US-09-504-231A-1703	Sequence 1703, Ap
847	15.4	1.0	36	10	US-09-274-553D-1703	Sequence 1703, Ap
848	15.4	1.0	37	10	US-09-027-287-12	Sequence 12, Appl
849	15.4	1.0	37	10	US-09-027-287-16	Sequence 16, Appl
850	15.4	1.0	37	10	US-09-252-656B-12	Sequence 12, Appl
851	15.4	1.0	37	10	US-09-252-656B-16	Sequence 16, Appl
852	15.4	1.0	38	9	US-09-864-785-830	Sequence 830, App
853	15.4	1.0	38	10	US-09-874-547-68	Sequence 68, Appl
854	15.4	1.0	38	10	US-09-874-547-77	Sequence 77, Appl
c 855	15.4	1.0	39	9	US-10-046-922-74	Sequence 74, Appl
856	15.4	1.0	39	10	US-09-874-547-23	Sequence 23, Appl
857	15.4	1.0	39	10	US-09-865-807-49	Sequence 49, Appl
c 858	15.4	1.0	40	10	US-09-790-417-211	Sequence 211, App
c 859	15.4	1.0	40	10	US-09-752-110A-12	Sequence 12, Appl
860	15.4	1.0	41	9	US-10-201-310-10	Sequence 10, Appl
861	15.4	1.0	42	9	US-09-943-722-96	Sequence 96, Appl
c 862	15.4	1.0	42	10	US-09-211-691-10	Sequence 10, Appl
863	15.4	1.0	42	10	US-09-853-379-9	Sequence 9, Appli
c 864	15.4	1.0	42	10	US-09-971-798-24	Sequence 24, Appl
865	15.4	1.0	43	9	US-09-832-658-13	Sequence 13, Appl
866	15.4	1.0	43	10	US-09-760-574-16	Sequence 16, Appl
867	15.4	1.0	43	10	US-09-855-266A-4	Sequence 4, Appli
c 868	15.4	1.0	44	9	US-09-896-594-3	Sequence 3, Appli
869	15.4	1.0	45	9	US-10-012-896-782	Sequence 782, App
870	15.4	1.0	45	9	US-09-895-793-782	Sequence 782, App
871	15.4	1.0	45	9	US-09-895-814-782	Sequence 782, App
872	15.4	1.0	45	9	US-09-995-847-26	Sequence 26, Appl
c 873	15.4	1.0	45	9	US-10-023-530-17	Sequence 17, Appl
c 874	15.4	1.0	45	9	US-10-211-069-45	Sequence 45, Appl
c 875	15.4	1.0	45	9	US-10-211-069-48	Sequence 48, Appl
c 876	15.4	1.0	45	9	US-10-007-132-15	Sequence 15, Appl
877	15.4	1.0	45	9	US-10-121-746-50	Sequence 50, Appl
878	15.4	1.0	45	9	US-09-977-797A-121	Sequence 121, App
c 879	15.4	1.0	45	10	US-09-742-693-3	Sequence 3, Appli
880	15.4	1.0	45	10	US-09-759-143-782	Sequence 782, App
881	15.4	1.0	45	10	US-09-780-669-782	Sequence 782, App
882	15.4	1.0	45	10	US-09-822-827-782	Sequence 782, App
883	15.4	1.0	46	7	US-08-911-824-115	Sequence 115, App
884	15.4	1.0	46	9	US-09-995-847-25	Sequence 25, Appl
c 885	15.4	1.0	46	9	US-09-900-379-69	Sequence 69, Appl
886	15.4	1.0	46	9	US-09-900-379-70	Sequence 70, Appl
c 887	15.4	1.0	46	10	US-09-848-164-69	Sequence 69, Appl
888	15.4	1.0	46	10	US-09-848-164-70	Sequence 70, Appl
889	15.4	1.0	47	9	US-09-853-526-59	Sequence 59, Appl
c 890	15.4	1.0	47	9	US-10-026-914-4	Sequence 4, Appli
891	15.4	1.0	47	9	US-09-880-464-15	Sequence 15, Appl
c 892	15.4	1.0	47	9	US-09-880-464-15	Sequence 15, Appl
893	15.4	1.0	47	10	US-09-785-632A-6	Sequence 6, Appli
c 894	15.4	1.0	47	10	US-09-785-632A-13	Sequence 13, Appl
895	15.4	1.0	47	10	US-09-901-484A-59	Sequence 59, Appl
c 896	15.4	1.0	47	10	US-09-975-408-56	Sequence 56, Appl
c 897	15.4	1.0	47	12	US-10-075-579-56	Sequence 56, Appl
898	15.4	1.0	49	8	US-08-978-633-10	Sequence 10, Appl
899	15.4	1.0	49	8	US-08-978-634-10	Sequence 10, Appl
900	15.4	1.0	49	8	US-08-978-637-10	Sequence 10, Appl
901	15.4	1.0	49	8	US-08-978-632-10	Sequence 10, Appl
902	15.4	1.0	50	9	US-09-905-291A-151	Sequence 151, App
903	15.4	1.0	50	9	US-09-902-853-151	Sequence 151, App
904	15.4	1.0	50	9	US-09-907-824-151	Sequence 151, App
905	15.4	1.0	50	9	US-09-907-841-151	Sequence 151, App
906	15.4	1.0	50	9	US-09-904-011-151	Sequence 151, App
907	15.4	1.0	50	9	US-09-906-742-151	Sequence 151, App
908	15.4	1.0	50	9	US-09-906-838-151	Sequence 151, App
909	15.4	1.0	50	9	US-09-907-613-151	Sequence 151, App
910	15.4	1.0	50	9	US-09-907-942-151	Sequence 151, App
911	15.4	1.0	50	9	US-09-904-820-151	Sequence 151, App
912	15.4	1.0	50	9	US-09-904-859-151	Sequence 151, App
913	15.4	1.0	50	9	US-09-909-204-151	Sequence 151, App
914	15.4	1.0	50	9	US-09-904-786-151	Sequence 151, App
915	15.4	1.0	50	9	US-09-906-646-151	Sequence 151, App
916	15.4	1.0	50	9	US-09-906-700-151	Sequence 151, App
917	15.4	1.0	50	9	US-09-902-903-151	Sequence 151, App
918	15.4	1.0	50	9	US-09-903-749A-151	Sequence 151, App
919	15.4	1.0	50	9	US-09-903-786-151	Sequence 151, App
920	15.4	1.0	50	10	US-09-179-536B-302	Sequence 302, App
921	15.4	1.0	50	10	US-09-909-320-151	Sequence 151, App
922	15.4	1.0	50	10	US-09-909-088B-151	Sequence 151, App
c 923	15.4	1.0	50	10	US-09-931-087A-11	Sequence 11, Appl
924	15.2	1.0	20	9	US-10-125-181-8	Sequence 8, Appli
925	15.2	1.0	25	10	US-09-866-108-3145	Sequence 3145, Ap
c 926	15.2	1.0	25	10	US-09-866-108-4469	Sequence 4469, Ap
c 927	15.2	1.0	25	10	US-09-866-108-4470	Sequence 4470, Ap
928	15.2	1.0	25	10	US-09-876-221-10	Sequence 10, Appl
c 929	15.2	1.0	29	10	US-09-810-502-30	Sequence 30, Appl
930	15.2	1.0	29	10	US-09-730-857-56	Sequence 56, Appl
c 931	15.2	1.0	29	10	US-09-730-857-57	Sequence 57, Appl
c 932	15.2	1.0	30	9	US-09-953-052-16	Sequence 16, Appl
c 933	15.2	1.0	30	9	US-09-953-052-23	Sequence 23, Appl
c 934	15.2	1.0	30	9	US-09-953-052-72	Sequence 72, Appl
935	15.2	1.0	30	9	US-10-033-297-156	Sequence 156, App
936	15.2	1.0	30	9	US-09-815-981-3	Sequence 3, Appli
937	15.2	1.0	30	9	US-09-940-244-156	Sequence 156, App
938	15.2	1.0	30	10	US-09-062-113-32	Sequence 32, Appl
c 939	15.2	1.0	30	10	US-09-062-113-33	Sequence 33, Appl
c 940	15.2	1.0	30	10	US-09-863-179-7	Sequence 7, Appli
c 941	15.2	1.0	31	9	US-09-773-599-8	Sequence 8, Appli
942	15.2	1.0	31	9	US-10-200-154-10	Sequence 10, Appl
943	15.2	1.0	31	9	US-09-912-263-110	Sequence 110, App
c 944	15.2	1.0	31	9	US-09-912-263-188	Sequence 188, App
945	15.2	1.0	31	9	US-09-912-263-210	Sequence 210, App
946	15.2	1.0	31	9	US-09-912-263-352	Sequence 352, App
947	15.2	1.0	31	9	US-09-912-263-371	Sequence 371, App
948	15.2	1.0	31	9	US-09-912-263-498	Sequence 498, App
949	15.2	1.0	31	10	US-09-801-274-40	Sequence 40, Appl
c 950	15.2	1.0	31	10	US-09-801-274-381	Sequence 381, App
c 951	15.2	1.0	31	10	US-09-801-274-386	Sequence 386, App
952	15.2	1.0	31	10	US-09-801-274-739	Sequence 739, App
c 953	15.2	1.0	31	10	US-09-801-274-1309	Sequence 1309, Ap
954	15.2	1.0	31	10	US-09-801-274-1485	Sequence 1485, Ap
c 955	15.2	1.0	31	10	US-09-801-274-1716	Sequence 1716, Ap
956	15.2	1.0	31	10	US-09-836-077-43	Sequence 43, Appl
957	15.2	1.0	31	10	US-09-954-043-10	Sequence 10, Appl
c 958	15.2	1.0	31	10	US-09-896-650A-7	Sequence 7, Appli
959	15.2	1.0	31	10	US-09-978-752-18	Sequence 18, Appl
960	15.2	1.0	32	9	US-10-066-127-11	Sequence 11, Appl
961	15.2	1.0	32	10	US-09-883-489-5	Sequence 5, Appli
c 962	15.2	1.0	33	8	US-08-913-699-2	Sequence 2, Appli
963	15.2	1.0	33	10	US-09-006-298-14	Sequence 14, Appl
c 964	15.2	1.0	33	10	US-09-736-743A-1	Sequence 1, Appli
c 965	15.2	1.0	33	10	US-09-850-716A-426	Sequence 426, App
c 966	15.2	1.0	33	10	US-09-912-787-15	Sequence 15, Appl
c 967	15.2	1.0	33	10	US-09-897-778-426	Sequence 426, App
c 968	15.2	1.0	33	12	US-10-014-326-1	Sequence 1, Appli

969	15.2	1.0	34	10	US-09-908-805B-55	Sequence 55, Appl
c 970	15.2	1.0	35	9	US-10-020-540A-7	Sequence 7, Appli
c 971	15.2	1.0	35	9	US-09-940-550A-7	Sequence 7, Appli
c 972	15.2	1.0	35	9	US-09-988-462-91	Sequence 91, Appl
c 973	15.2	1.0	35	10	US-09-872-153-27	Sequence 27, Appl
974	15.2	1.0	36	9	US-10-056-414-577	Sequence 577, App
c 975	15.2	1.0	36	9	US-09-927-122-49	Sequence 49, Appl
c 976	15.2	1.0	36	10	US-09-504-231A-2453	Sequence 2453, Ap
c 977	15.2	1.0	36	10	US-09-504-231A-2664	Sequence 2664, Ap
c 978	15.2	1.0	36	10	US-09-274-553D-2453	Sequence 2453, Ap
c 979	15.2	1.0	36	10	US-09-274-553D-2664	Sequence 2664, Ap
c 980	15.2	1.0	36	10	US-09-824-924-2	Sequence 2, Appli
981	15.2	1.0	36	12	US-10-116-288-10	Sequence 10, Appl
c 982	15.2	1.0	37	9	US-09-864-785-1737	Sequence 1737, Ap
c 983	15.2	1.0	37	9	US-09-918-696-43	Sequence 43, Appl
984	15.2	1.0	37	9	US-09-918-696-44	Sequence 44, Appl
c 985	15.2	1.0	37	10	US-09-778-168-16	Sequence 16, Appl
c 986	15.2	1.0	37	10	US-09-778-175-16	Sequence 16, Appl
c 987	15.2	1.0	37	10	US-09-335-218-16	Sequence 16, Appl
988	15.2	1.0	37	10	US-09-179-536B-245	Sequence 245, App
c 989	15.2	1.0	38	9	US-09-864-785-742	Sequence 742, App
990	15.2	1.0	38	9	US-09-864-785-1133	Sequence 1133, Ap
991	15.2	1.0	38	10	US-09-179-536B-246	Sequence 246, App
992	15.2	1.0	38	10	US-09-874-547-75	Sequence 75, Appl
c 993	15.2	1.0	38	10	US-09-870-203A-23	Sequence 23, Appl
994	15.2	1.0	38	10	US-09-870-203A-24	Sequence 24, Appl
c 995	15.2	1.0	39	9	US-09-934-060A-7	Sequence 7, Appli
996	15.2	1.0	39	9	US-10-000-512-24	Sequence 24, Appl
c 997	15.2	1.0	39	9	US-09-977-418-85	Sequence 85, Appl
c 998	15.2	1.0	39	9	US-09-940-244-204	Sequence 204, App
c 999	15.2	1.0	39	9	US-09-940-244-205	Sequence 205, App
c1000	15.2	1.0	39	10	US-09-473-872-30	Sequence 30, Appl

ALIGNMENTS

```
RESULT 1
US-09-782-650-16
; Sequence 16, Application US/09782650
; Patent No. US20020019350A1
; GENERAL INFORMATION:
;  APPLICANT: Levine, Arnold J.
;  APPLICANT:  Mitterer, Artur
;  APPLICANT:  Falkner, Falko-Guenter
;  APPLICANT:  Scheiflinger, Friedrich
;  APPLICANT:  Dorner, Friedrich
;  APPLICANT:  Edwards LifeSciences Corporation
;  TITLE OF INVENTION: Targeted Angiogenesis
;  FILE REFERENCE: 20553D-000611US
;  CURRENT APPLICATION NUMBER: US/09/782,650
;  CURRENT FILING DATE:  2001-02-12
;  PRIOR APPLICATION NUMBER: US 09/324,079
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: US 09/327,045
;  PRIOR FILING DATE: 1999-06-07
;  PRIOR APPLICATION NUMBER: PCT/US00/14988
;  PRIOR FILING DATE: 2000-05-31
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:annealed
;   OTHER INFORMATION: oligonucleotide
US-09-782-650-16

  Query Match             2.0%;  Score 31.4;  DB 10;  Length 50;
  Best Local Similarity   85.4%;  Pred. No. 1.2e+03;
  Matches   35;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   1341 GCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGC 1381
          ||||||| | |||||||||||| | | |||| |||||||||
Db      7 GCGGCGGCGGCAGCGGCGGCGGCGGCAGCGGCGGCGGCGGC 47


RESULT 2
US-09-883-848A-37/c
; Sequence 37, Application US/09883848A
; Publication No. US20030022819A1
; GENERAL INFORMATION:
;  APPLICANT: Ling, L.
;  APPLICANT:  Sanicola-Nadel, M.
;  TITLE OF INVENTION: ANGIOGENESIS-MODULATING COMPOSITIONS AND USES
;  FILE REFERENCE: CIBT-P01-119
;  CURRENT APPLICATION NUMBER: US/09/883,848A
;  CURRENT FILING DATE:  2001-06-18
;  PRIOR APPLICATION NUMBER: 60/211,919
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide
US-09-883-848A-37

  Query Match             1.4%;  Score 22;  DB 9;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+04;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    221 TGCGGACCGGGCAGGGGGTTCG 242
          |||||||||||||||||||||||
Db     22 TGCGGACCGGGCAGGGGGTTCG 1


RESULT 3
US-09-828-034-7/c
; Sequence 7, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
;  APPLICANT: Zhong, Weidong
;  APPLICANT:  Hong, Zhi
;  APPLICANT:  Ferrari, Eric
;  TITLE OF INVENTION: HCV REPLICASE COMPLEXES
;  FILE REFERENCE: IN01165
;  CURRENT APPLICATION NUMBER: US/09/828,034
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: U.S. 60/195,852
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 30
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-7

  Query Match             1.4%;  Score 22;  DB 10;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 6.2e+04;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   1546 GGGGGCCGGGGGAGGGGCGCGGGAGGGGGC 1575
          |||||| ||||  |||||| ||| ||||||
Db     30 GGGGGCGGGGGCGGGGGCGGGGGCGGGGGC 1


RESULT 4
US-10-006-856A-151
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; Sequence 151, Application US/10006856A
; Publication No. US20030044841A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C14
;  CURRENT APPLICATION NUMBER: US/10/006,856A
;  CURRENT FILING DATE:  2002-05-10
;  NUMBER OF SEQ ID NOS: 477
;  Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 151
;   LENGTH: 45
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-856A-151

  Query Match             1.4%;  Score 21.4;  DB 9;  Length 45;
  Best Local Similarity   71.8%;  Pred. No. 8.3e+04;
  Matches   28;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    763 GGTGCACCTGGAGCAGGGCGGCACCAAGCTGGTGAAGGA 801
          | |||  | | | || ||| | || || ||||||||||
Db      4 GATGCCACAGTATCAAGGCAGGACAAAACTGGTGAAGGA 42


RESULT 5
US-10-135-984-6
; Sequence 6, Application US/10135984
; Publication No. US20020182595A1
; GENERAL INFORMATION:
;  APPLICANT: Matthew D. Weitzman
;  APPLICANT:  Anton J. Cathomen
;  TITLE OF INVENTION: METHOD OF IDENTIFYING CELLULAR
;  TITLE OF INVENTION:  REGULATORS OF ADENO-ASSOCIATED VIRUS (AAV)
;  FILE REFERENCE: SALKINS.041A
;  CURRENT APPLICATION NUMBER: US/10/135,984
;  CURRENT FILING DATE:  2002-08-05
;  PRIOR APPLICATION NUMBER: 60/286951
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 45
;   TYPE: DNA
;   ORGANISM: adeno-associated virus
US-10-135-984-6

  Query Match             1.3%;  Score 20.8;  DB 9;  Length 45;
  Best Local Similarity   70.0%;  Pred. No. 1.1e+05;
  Matches   28;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy      1 GCGAGGCAGCCAGCGAGGGAGAGAGCGAGCGGGCGAGCCG 40
          | |||  ||| |||| |   | |||||||||| ||| || |
Db      5 GTGAGCGAGCGAGCGCGCAGGTGAGCGAGCGAGCGCGCAG 44


RESULT 6
US-10-135-984-4
; Sequence 4, Application US/10135984
; Publication No. US20020182595A1
; GENERAL INFORMATION:
;  APPLICANT: Matthew D. Weitzman
;  APPLICANT:  Anton J. Cathomen
;  TITLE OF INVENTION: METHOD OF IDENTIFYING CELLULAR
;  TITLE OF INVENTION:  REGULATORS OF ADENO-ASSOCIATED VIRUS (AAV)
;  FILE REFERENCE: SALKINS.041A
;  CURRENT APPLICATION NUMBER: US/10/135,984
;  CURRENT FILING DATE:  2002-08-05
;  PRIOR APPLICATION NUMBER: 60/286951
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: adeno-associated virus
US-10-135-984-4

  Query Match             1.3%;  Score 20.8;  DB 9;  Length 46;
  Best Local Similarity   70.0%;  Pred. No. 1.1e+05;
  Matches   28;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy      1 GCGAGGCAGCCAGCGAGGGAGAGAGCGAGCGGGCGAGCCG 40
          | |||  ||| |||| |   | |||||||||| ||| || |
Db      6 GTGAGCGAGCGAGCGCGCAGGTGAGCGAGCGAGCGCGCAG 45


RESULT 7
US-10-135-984-5/c
; Sequence 5, Application US/10135984
; Publication No. US20020182595A1
; GENERAL INFORMATION:
;  APPLICANT: Matthew D. Weitzman
;  APPLICANT:  Anton J. Cathomen
;  TITLE OF INVENTION: METHOD OF IDENTIFYING CELLULAR
;  TITLE OF INVENTION:  REGULATORS OF ADENO-ASSOCIATED VIRUS (AAV)
;  FILE REFERENCE: SALKINS.041A
;  CURRENT APPLICATION NUMBER: US/10/135,984
;  CURRENT FILING DATE:  2002-08-05
;  PRIOR APPLICATION NUMBER: 60/286951
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: adeno-associated virus
US-10-135-984-5

  Query Match             1.3%;  Score 20.8;  DB 9;  Length 46;
  Best Local Similarity   70.0%;  Pred. No. 1.1e+05;
  Matches   28;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy      1 GCGAGGCAGCCAGCGAGGGAGAGAGCGAGCGGGCGAGCCG 40
          | |||  ||| |||| |   | |||||||||| ||| || |
Db     45 GTGAGCGAGCGAGCGCGCAGGTGAGCGAGCGAGCGCGCAG 6


RESULT 8
US-10-135-984-7/c
; Sequence 7, Application US/10135984
; Publication No. US20020182595A1
; GENERAL INFORMATION:
;  APPLICANT: Matthew D. Weitzman
;  APPLICANT:  Anton J. Cathomen
;  TITLE OF INVENTION: METHOD OF IDENTIFYING CELLULAR
;  TITLE OF INVENTION:  REGULATORS OF ADENO-ASSOCIATED VIRUS (AAV)
;  FILE REFERENCE: SALKINS.041A
;  CURRENT APPLICATION NUMBER: US/10/135,984
;  CURRENT FILING DATE:  2002-08-05
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;  PRIOR APPLICATION NUMBER: 60/286951
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 46
;   TYPE: DNA
;   ORGANISM: adeno-associated virus
US-10-135-984-7

  Query Match             1.3%;  Score 20.8;  DB 9;  Length 46;
  Best Local Similarity   70.0%;  Pred. No. 1.1e+05;
  Matches   28;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy       1 GCGAGGCAGCCAGCGAGGGAGAGAGCGAGCGGGCGAGCCG 40
           | |||  ||| |||| |   | |||||||| ||| || |
Db      45 GTGAGCGAGCGAGCGCGCAGGTGAGCGAGCGAGCGCGCAG 6


RESULT 9
US-09-888-326-172/c
; Sequence 172, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
;  APPLICANT: Weiner, George
;  APPLICANT:  Hartmann, Gunther
;  TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
;  TITLE OF INVENTION:  Cell Lysis and Treating Cancer
;  FILE REFERENCE: C1039/7052 (AWS)
;  CURRENT APPLICATION NUMBER: US/09/888,326
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: US 60/213,346
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 848
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 172
;   LENGTH: 35
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-172

  Query Match             1.3%;  Score 20.4;  DB 9;  Length 35;
  Best Local Similarity   80.0%;  Pred. No. 1.2e+05;
  Matches   24;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    1545 GGGGGGCCGGGGGAGGGGCGCGGGAGGGGG 1574
           ||||||  ||||| |||| | ||| |||||
Db      34 GGGGGGGGGGGGGGGGGGGGGGGGGGGGG 5


RESULT 10
US-10-027-961A-14
; Sequence 14, Application US/10027961A
; Publication No. US20030032789A1
; GENERAL INFORMATION:
;  APPLICANT: O'NEILL, GARY P.
;  APPLICANT:  MANCINI, JOSEPH A.
;  TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
;  TITLE OF INVENTION:  CYCLOOXYGENASE-2
;  FILE REFERENCE: 19029PCADA
;  CURRENT APPLICATION NUMBER: US/10/027,961A
;  CURRENT FILING DATE:  2001-10-25
;  PRIOR APPLICATION NUMBER: 09/599,781
;  PRIOR FILING DATE: 2000-06-21
;  PRIOR APPLICATION NUMBER: 08/930,589
;  PRIOR FILING DATE: 1996-02-22
;  PRIOR APPLICATION NUMBER: PCT/CA94/00501
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: 08/084,033
;  PRIOR FILING DATE: 1993-09-27
;  PRIOR APPLICATION NUMBER: 08/064,271
;  PRIOR FILING DATE: 1993-05-06
;  PRIOR APPLICATION NUMBER: 07/994,760
;  PRIOR FILING DATE: 1992-12-22
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 41
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-961A-14

  Query Match             1.3%;  Score 20.4;  DB 9;  Length 41;
  Best Local Similarity   71.1%;  Pred. No. 1.3e+05;
  Matches   27;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     183 TCCTCGTCTCCTCGCTGCTGGTATGCTCGGGACTGGCG 220
           | |||| |  | | |||||| | ||| |||  ||||||
Db       3 TGCTCGCCCGCGCCCTGCTGCTGTGCGCGGTCCTGGCG 40


RESULT 11
US-09-740-002-9
; Sequence 9, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
;  APPLICANT: BRAMS, PETER
;  APPLICANT:  MORROW, PHILLIP
;  TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
;  TITLE OF INVENTION:  SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
;  TITLE OF INVENTION:  MANUFACTURE AND THERAPEUTIC USE THEREOF
;  FILE REFERENCE: 037003-0275759
;  CURRENT APPLICATION NUMBER: US/09/740,002
;  CURRENT FILING DATE:  2000-12-20
;  PRIOR APPLICATION NUMBER: 09/335,697
;  PRIOR FILING DATE: 1999-06-18
;  PRIOR APPLICATION NUMBER: 08/488,376
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 49
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-740-002-9

  Query Match             1.3%;  Score 20.4;  DB 10;  Length 49;
  Best Local Similarity   71.1%;  Pred. No. 1.3e+05;
  Matches   27;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

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Db       2 GAGAGAGAGAGAGAGAGCCAGATACACGATGTGAAA 39


RESULT 12
US-10-072-152-32
; Sequence 32, Application US/10072152
; Patent No. US20020142438A1
; GENERAL INFORMATION:
;  APPLICANT: Andersen, Lene N.
;  APPLICANT:  Schulein, Martin
;  APPLICANT:  Lange, Niels E.
;  APPLICANT:  Bjornvad, Mads E.
;  APPLICANT:  Moller, Soren
;  APPLICANT:  Glad, Sanne O. S.
;  APPLICANT:  Kauppinen, Markus S.
;  APPLICANT:  Schnorr, Kirk
;  APPLICANT:  Kongsbak, Lars
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;  TITLE OF INVENTION: No. US20020142438A1el Pectate Lyases
;  FILE REFERENCE: 5378.200-US
;  CURRENT APPLICATION NUMBER: US/10/072,152
;  CURRENT FILING DATE:  2002-02-07
;  PRIOR APPLICATION NUMBER: US/09/198,955
;  PRIOR FILING DATE: 1998-11-24
;  PRIOR APPLICATION NUMBER: 1343/97
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 1344/97
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/067,249
;  PRIOR FILING DATE: 1997-12-02
;  PRIOR APPLICATION NUMBER: 60/067,240
;  PRIOR FILING DATE: 1997-12-02
;  PRIOR APPLICATION NUMBER: 09/073,684
;  PRIOR FILING DATE: 1998-05-06
;  PRIOR APPLICATION NUMBER: 09/184,217
;  PRIOR FILING DATE: 1998-11-02
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 48
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-072-152-32

  Query Match             1.3%;  Score 20.2;  DB 12;  Length 48;
  Best Local Similarity   68.3%;  Pred. No. 1.4e+05;
  Matches   28;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

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RESULT 13
US-09-992-598-122
; Sequence 122, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C20
;  CURRENT APPLICATION NUMBER: US/09/992,598
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/065186
;  PRIOR FILING DATE: 1997-11-12
;  PRIOR APPLICATION NUMBER: 60/065311
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;  PRIOR FILING DATE: 1997-11-24
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;  PRIOR FILING DATE: 1998-02-25
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 20; DB 9; Length 45;
Best Local Similarity 65.9%; Pred. No. 1.5e+05;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Db       2 GCTGCTCCTGCTGCCGCCGCTGCTGCTGGGGGCCTTCCCGCCGG 45
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RESULT 14
US-09-989-293A-122
; Sequence 122, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone ;
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 20; DB 9; Length 45;
Best Local Similarity 65.9%; Pred. No. 1.5e+05;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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RESULT 15
US-09-989-735-122
; Sequence 122, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
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; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
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Query Match 1.3%; Score 20; DB 9; Length 45;
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Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
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;  APPLICANT:  Desnoyers,Luc
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;  APPLICANT:  Gerber,Hanspeter
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;  APPLICANT:  Goddard,Audrey
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;  APPLICANT:  Williams, P. Mickey
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;  TITLE OF INVENTION:  Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 20; DB 9; Length 45;
Best Local Similarity 65.9%; Pred. No. 1.5e+05;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy   1400 GCTCCAGGTGCTGCCGACGCTCCGGGTGCGGGGGCCACCGCGGG 1443
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Db      2 GCTGCTCCTGCTGCCGCCGCTGCTGCTGGGGGCCTTCCCGCCGG 45
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RESULT 18
US-09-990-436-122
; Sequence 122, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C14
; CURRENT APPLICATION NUMBER: US/09/990,436
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 20; DB 9; Length 45;
Best Local Similarity 65.9%; Pred. No. 1.5e+05;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy    1400 GCTCCAGGTGCTGCCGACGCTCCGGGTGCGGGGGCCACCGCGGG 1443
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Db       2 GCTGCTCCTGCTGCCGCCGCTGCTGCTGGGGGCCTTCCCGCCGG 45
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RESULT 19
US-09-991-181-122
; Sequence 122, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/075945
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 20; DB 9; Length 45;
Best Local Similarity 65.9%; Pred. No. 1.5e+05;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy   1400 GCTCCAGGTGCTGCCGACGCTCCGGGTGCGGGGGCCACCGCGGG 1443
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Db      2 GCTGCTCCTGCTGCCGCCGCTGCTGCTGGGGGCCTTCCCGCCGG 45
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RESULT 20
US-09-993-687-122
; Sequence 122, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C11
; CURRENT APPLICATION NUMBER: US/09/993,687
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-11-13
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; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
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; PRIOR APPLICATION NUMBER: 60/089948
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; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 20; DB 9; Length 45;
Best Local Similarity 65.9%; Pred. No. 1.5e+05;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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RESULT 21
US-09-989-734-122
; Sequence 122, Application US/09989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.

; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C64
; CURRENT APPLICATION NUMBER: US/09/989,734
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 20; DB 9; Length 45;
Best Local Similarity 65.9%; Pred. No. 1.5e+05;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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RESULT 22
US-09-997-653-122
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; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C38
; CURRENT APPLICATION NUMBER: US/09/997,653
; CURRENT FILING DATE: 2001-11-15
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 20; DB 9; Length 45;
Best Local Similarity 65.9%; Pred. No. 1.5e+05;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Db      2 GCTGCTCCTGCTGCCGCCGCTGCTGCTGGGGGCCTTCCCGCCGG 45
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RESULT 23
US-09-993-667-122
; Sequence 122, Application US/09993667
; Publication No. US20030022187A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C4
; CURRENT APPLICATION NUMBER: US/09/993,667

; CURRENT FILING DATE: 2001-11-14
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; PRIOR APPLICATION NUMBER: 60/088326
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; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
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;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

  Query Match             1.3%;  Score 20;  DB 9;  Length 45;
  Best Local Similarity   65.9%;  Pred. No. 1.5e+05;
  Matches   29;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

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; Sequence 35, Application US/10211069
; Publication No. US20030021797A1
; GENERAL INFORMATION:
;  APPLICANT: DATTA, Syamal K
;  APPLICANT:  KALIYAPERUMAL, Arunan
;  TITLE OF INVENTION: LOCALIZATION OF MAJOR PEPTIDE AUTOEPITOPES FOR NUCLEOSOME SPECIF
;  TITLE OF INVENTION:  IC T CELLS OF SYSTEMIC LUPUS ERYTHEMATOSUS
;  FILE REFERENCE: 290-13U1 (53662-5017
;  CURRENT APPLICATION NUMBER: US/10/211,069
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: US/09/561,490
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: US 60/131,448
;  PRIOR FILING DATE: 1999-04-28
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 45
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Histone fragment
US-10-211-069-35

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RESULT 25
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; Sequence 122, Application US/09990438
; Publication No. US20030027754A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C3
;  CURRENT APPLICATION NUMBER: US/09/990,438
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.3%; Score 20; DB 9; Length 45;
Best Local Similarity 65.9%; Pred. No. 1.5e+05;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Search completed: March 14, 2003, 01:18:09
Job time : 167 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 13, 2003, 21:47:38 ; Search time 2407 Seconds
(without alignments)
10604.108 Million cell updates/sec

Title: US-10-001-844-3
Perfect score: 1576
Sequence: 1 gcgaggcagccagcgaggga.....gaggggcgcgggaggggccc 1576

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST:*
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2: em_esthum:*
3: em_estin:*
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8: em_htc:*
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23: em_gss_mam:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	25	1.6	45	13	BI772215	BI772215 603056165
c	4	25	1.6	49	9	AA842027	AA842027 MBAFCF2D0
	5	25	1.6	49	9	AI813244	AI813244 3G2 Pine
c	6	25	1.6	49	10	AV833587	AV833587 AV833587
	7	24.4	1.5	49	12	BF970690	BF970690 602273861
c	8	24.2	1.5	47	10	AV947640	AV947640 AV947640
c	9	23.8	1.5	45	13	BJ000572	BJ000572 BJ000572
	10	23.8	1.5	46	9	AI701058	AI701058 wc78c06.x
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c	12	23.6	1.5	47	10	AV949200	AV949200 AV949200
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c	15	23.6	1.5	47	17	AZ862836	AZ862836 2M0170N09
c	16	23.6	1.5	47	17	AZ864870	AZ864870 2M0174M10
	17	23.4	1.5	45	9	AL676139	AL676139 AL676139.
	18	23.4	1.5	49	17	AZ335579	AZ335579 1M0065A01
	19	23.4	1.5	50	14	BQ577141	BQ577141 PfESToab1
c	20	23.2	1.5	44	10	AV672475	AV672475 AV672475
c	21	22.6	1.4	49	9	AA977986	AA977986 oq55a06.s
c	22	22.6	1.4	50	9	AU103717	AU103717 AU103717
	23	22.4	1.4	50	12	BG078033	BG078033 H3022G12-
	24	22.4	1.4	50	14	BQ807914	BQ807914 NISC_kk11
	25	22.2	1.4	43	13	BI547391	BI547391 603197282
	26	22.2	1.4	43	17	AZ345546	AZ345546 1M0080C14
	27	22.2	1.4	44	10	AV833550	AV833550 AV833550
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c	33	22	1.4	35	17	AZ389253	AZ389253 1M0149K07
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	53	22	1.4	43	17	AZ407933	AZ407933 1M0178G23
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c	55	22	1.4	43	17	AZ666812	AZ666812 1M0549O12
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AZ946537 2M0208E19
AZ949191 2M0212K02

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	886	17.6	1.1	34	9	AA748312
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	889	17.6	1.1	37	9	AA873697
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	893	17.6	1.1	39	17	AZ486481
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c	895	17.6	1.1	40	17	AZ615880
	896	17.6	1.1	41	14	R19040
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c	898	17.6	1.1	42	17	AZ983516
	899	17.6	1.1	43	9	AI282953
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c	906	17.6	1.1	46	9	AI582875
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	908	17.6	1.1	46	13	BI829941
	909	17.6	1.1	46	17	BH636244
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c	922	17.6	1.1	50	9	AU102407
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c	933	17.6	1.1	50	9	AU102797
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c	936	17.6	1.1	50	9	AU102946
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c	938	17.6	1.1	50	9	AU103430
c	939	17.6	1.1	50	9	AU103481
c	940	17.6	1.1	50	9	AU103661
	941	17.6	1.1	50	9	AU103716
c	942	17.6	1.1	50	9	AU104519
	943	17.6	1.1	50	9	AU104581
	944	17.6	1.1	50	9	AU104734
	945	17.6	1.1	50	9	AU104801
	946	17.6	1.1	50	9	AU104810
c	947	17.6	1.1	50	9	AU104848
	948	17.6	1.1	50	9	AU105173
	949	17.6	1.1	50	9	AU105193
c	950	17.6	1.1	50	9	AU105246
c	951	17.6	1.1	50	9	AU106535
c	952	17.6	1.1	50	9	AU106561
	953	17.6	1.1	50	9	AU106873
c	954	17.6	1.1	50	9	AU107071
	955	17.6	1.1	50	9	AU107368

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AZ486481 1M0314H03
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BE899162 601681959
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AI282953 qt82g09.x
BH619995 1007063H1
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AI582875 ts07a07.x
AI884025 fc72c11.x
BI829941 603080075
BH636244 1008010A0
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AZ497723 1M0334L09
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AA478678 zv19g04.r
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957	17.6	1.1	50	9	AU107676	AU107676 AU107676
c 958	17.6	1.1	50	9	AU107945	AU107945 AU107945
959	17.6	1.1	50	13	BI830809	BI830809 603080922
960	17.6	1.1	50	13	BM522862	BM522862 sam98g09.
961	17.4	1.1	27	17	AZ342261	AZ342261 1M0075D15
c 962	17.4	1.1	27	17	AZ427735	AZ427735 1M0209I20
963	17.4	1.1	27	17	AZ443194	AZ443194 1M0237E17
c 964	17.4	1.1	27	17	AZ470448	AZ470448 1M0284H04
c 965	17.4	1.1	27	17	AZ481721	AZ481721 1M0306J12
966	17.4	1.1	27	17	AZ496388	AZ496388 1M0332J14
967	17.4	1.1	27	17	AZ638528	AZ638528 1M0498A04
c 968	17.4	1.1	27	17	AZ657419	AZ657419 1M0533O06
c 969	17.4	1.1	27	17	AZ782519	AZ782519 2M0022O22
c 970	17.4	1.1	27	17	AZ833127	AZ833127 2M0115C06
c 971	17.4	1.1	28	17	AZ872959	AZ872959 2M0186F03
c 972	17.4	1.1	29	17	AZ642459	AZ642459 1M0505D06
973	17.4	1.1	31	9	AA878823	AA878823 of87c04.s
c 974	17.4	1.1	33	17	AZ793186	AZ793186 2M0046A13
c 975	17.4	1.1	34	17	AZ825014	AZ825014 2M0100A06
976	17.4	1.1	36	17	AZ599457	AZ599457 1M0414L14
c 977	17.4	1.1	38	12	BF131669	BF131669 601820610
c 978	17.4	1.1	38	17	AZ424085	AZ424085 1M0203B05
979	17.4	1.1	40	9	AA811470	AA811470 ob83d02.s
c 980	17.4	1.1	40	9	AI800161	AI800161 tr23b08.x
c 981	17.4	1.1	40	9	AA258320	AA258320 zr59f02.s
982	17.4	1.1	40	17	AZ645161	AZ645161 1M0510N19
c 983	17.4	1.1	43	9	AL780039	AL780039 AL780039
984	17.4	1.1	43	13	BI916603	BI916603 603178534
985	17.4	1.1	43	17	AZ801137	AZ801137 2M0059A05
c 986	17.4	1.1	45	17	AZ767751	AZ767751 1M0567A14
987	17.4	1.1	45	17	CNS07EY5	AL607775 Anopheles
c 988	17.4	1.1	46	9	AA890005	AA890005 aj89h03.s
989	17.4	1.1	46	9	AI583420	AI583420 tr96g06.x
990	17.4	1.1	46	9	AI631068	AI631068 tz32b08.x
c 991	17.4	1.1	46	9	AI667536	AI667536 fc41e06.x
c 992	17.4	1.1	46	13	BG914443	BG914443 602813175
993	17.4	1.1	46	14	H68899	H68899 yr86a03.r1
c 994	17.4	1.1	46	17	BH840725	BH840725 KG06941-5
995	17.4	1.1	47	17	AZ331661	AZ331661 1M0059E13
996	17.4	1.1	47	17	BH806710	BH806710 1008075B0
997	17.4	1.1	48	12	BF529639	BF529639 602043868
c 998	17.4	1.1	49	9	AA914273	AA914273 vy99a03.r
999	17.4	1.1	49	9	AI414486	AI414486 ma08f03.x
c1000	17.4	1.1	49	14	BQ417691	BQ417691 ik44c06.x

ALIGNMENTS

RESULT 1
BI462985
LOCUS BI462985 43 bp mRNA linear EST 21-AUG-2001
DEFINITION 603204504F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5270424 5', mRNA sequence.
ACCESSION BI462985
VERSION BI462985.1 GI:15253641
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11682 row: g column: 01
High quality sequence stop: 43.
FEATURES Location/Qualifiers
source 1. .43
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5270424"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 5 a 8 c 28 g 2 t
ORIGIN

Query Match 1.7%; Score 26.2; DB 13; Length 43;
Best Local Similarity 79.5%; Pred. No. 2.2e+05;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy   1344 GCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCG 1382
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Db      2 GCGGGGGAAGCGGCGGCGGGGCCCGGGAGAGGGGTGGCG 40
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RESULT 2
AZ374770/c
LOCUS AZ374770 50 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0127I18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0127I18 R, DNA sequence.
ACCESSION AZ374770
VERSION AZ374770.1 GI:10488470
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0127 row: I column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 50.
FEATURES Location/Qualifiers
source 1. .50
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0127I18"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 0 a 25 c 0 g 25 t
ORIGIN

Query Match 1.6%; Score 26; DB 17; Length 50;
Best Local Similarity 70.0%; Pred. No. 2.5e+05;
Matches 35; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 19 GAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGA 68
||||||| ||| | | ||| ||| ||| || || || | |||||||
Db 50 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 1

RESULT 3
BI772215
LOCUS BI772215 45 bp mRNA linear EST 25-SEP-2001
DEFINITION 603056165F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5205425 5', mRNA sequence.
ACCESSION BI772215
VERSION BI772215.1 GI:15763793
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 45)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11515 row: b column: 18
High quality sequence stop: 45.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5205425"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
BASE COUNT 6 a 11 c 25 g 3 t
ORIGIN

Query Match 1.6%; Score 25; DB 13; Length 45;
Best Local Similarity 75.6%; Pred. No. 3.8e+05;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1342 CGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCG 1382
|||||| | || | |||| ||| |||| ||||||||||
Db 5 CGGCGGTGGCAAGAGTAGCGGTGACGGCGGCGGCGGCGGCG 45

RESULT 4
AA842027/c
LOCUS AA842027 49 bp mRNA linear EST 02-MAR-1998
DEFINITION MBAFCF2D03T3 Brugia malayi adult female cDNA (SAW96MLW-BmAF) Brugia malayi cDNA clone AFCF2D03 5', mRNA sequence.
ACCESSION AA842027
VERSION AA842027.1 GI:2923363
KEYWORDS EST.
SOURCE Brugia malayi.
ORGANISM Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.
REFERENCE 1 (bases 1 to 49)
AUTHORS Blaxter,M.L., Waterfall,M., Daub,J., Lizotte,M., Baron,L. and Jones,S.J.
TITLE Genes expressed in adult female Brugia malayi
JOURNAL Unpublished (1996)
COMMENT Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JT, UK.
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
The ABI trace of this sequence can be viewed at
http://www.sanger.ac.uk/brugia/AFC/MBAFCF2D03T3.html
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .49
/organism="Brugia malayi"
/db_xref="taxon:6279"
/clone="AFCF2D03"
/clone_lib="Brugia malayi adult female cDNA (SAW96MLW-BmAF)"
/sex="female"
/dev_stage="adult"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from approximately 50 adult females isolated from the peritoneal cavity of jirds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 5 x 10E6 independent recombinants and the average insert size is ~900bp.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT 0 a 23 c 2 g 24 t
ORIGIN

Query Match 1.6%; Score 25; DB 9; Length 49;
Best Local Similarity 69.4%; Pred. No. 3.8e+05;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 12 AGCGAGGGAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGC 60

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Db     49 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCAC 1


RESULT 5
AI813244
LOCUS       AI813244                  49 bp    mRNA    linear   EST 08-JUL-1999
DEFINITION  3G2 Pine Lambda Zap Xylem library Pinus taeda cDNA, mRNA sequence.
ACCESSION   AI813244
VERSION     AI813244.1  GI:5424459
KEYWORDS    EST.
SOURCE      loblolly pine.
  ORGANISM  Pinus taeda
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Whetten,R.W., Kinlaw,C.S., Retzel,E. and Sederoff,R.R.
  TITLE     The Pine Gene Discovery Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Ross Whetten
            Forest Biotechnology Group
            North Carolina State University
            Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
            ,NC, 27695-8008
            Tel: 919-515-7800
            Fax: 919-515-7801
            Email: rosswhet@unity.ncsu.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Pinus taeda"
                     /db_xref="taxon:3352"
                     /clone_lib="Pine Lambda Zap Xylem library"
                     /tissue_type="differentiating xylem"
                     /note="Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI;
                     Differentiating xylem was collected from the main stem of
                     a 35-year old loblolly pine tree harvested during the
                     growing season. RNA isolation and library preparation
                     followed the methods of Allona et al., PNAS 95:9693-8,
                     1998"
BASE COUNT       24 a      0 c     25 g      0 t
ORIGIN

  Query Match             1.6%;  Score 25;  DB 9;  Length 49;
  Best Local Similarity   69.4%;  Pred. No. 3.8e+05;
  Matches   34;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy      21 GAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGAG 69
           ||||| ||| | | |||   ||| |||  || || || |  ||||||||
Db       1 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 49


RESULT 6
AV833587/c
LOCUS       AV833587                  49 bp    mRNA    linear   EST 22-JUN-2001
DEFINITION  AV833587 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
            vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA
            clone bags16a08, mRNA sequence.
ACCESSION   AV833587
VERSION     AV833587.1  GI:14525676
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare.
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Sato,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Kazuhiro Sato
            Research Institute for Bioresources
            Okayama University, Barley Germplasm Center
            Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
            Email: kazsato@rib.okayama-u.ac.jp,
            URL:http://www.rib.okayama-u.ac.jp/barley/
            Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
            submission;
            database:http://www.shigen.nig.ac.jp/barley/Barley.html.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Hordeum vulgare subsp. vulgare"
                     /cultivar="Haruna Nijo"
                     /db_xref="taxon:112509"
                     /clone="bags16a08"
                     /clone_lib="K. Sato unpublished cDNA library: Hordeum
                     vulgare subsp. vulgare shoots germination"
                     /tissue_type="shoots"
                     /dev_stage="germination"
BASE COUNT       0 a      25 c      0 g     24 t
ORIGIN

  Query Match             1.6%;  Score 25;  DB 10;  Length 49;
  Best Local Similarity   69.4%;  Pred. No. 3.8e+05;
  Matches   34;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy      21 GAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGAG 69
           ||||| ||| | | |||   ||| |||  || || || |  ||||||||
Db      49 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1


RESULT 7
BF970690
LOCUS       BF970690                  49 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION  602273861F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4361943 5',
            mRNA sequence.
ACCESSION   BF970690
VERSION     BF970690.1  GI:12337905
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10005  row: i  column: 16
            High quality sequence stop: 49.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4361943"
                     /clone_lib="NIH_MGC_84"
                     /tissue_type="adrenal cortex carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
                     primed. Average insert size 1.229 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT       8 a      12 c     25 g      4 t
ORIGIN

  Query Match             1.5%;  Score 24.4;  DB 12;  Length 49;
  Best Local Similarity   73.8%;  Pred. No. 5e+05;
```

```
  Matches   31;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   1341 GCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCG 1382
          || ||   | | ||||||||||| | | ||  ||||||||||||
Db      1 GCAGCTACGGCGGCGGCGGCGGTGGCGGCTAGGGCGGCGGCG 42


RESULT 8
AV947640/c
LOCUS       AV947640                  47 bp    mRNA    linear   EST 14-MAR-2002
DEFINITION  AV947640 Nori Satoh unpublished cDNA library, young adult Ciona
            intestinalis cDNA clone ciad01g16 5', mRNA sequence.
ACCESSION   AV947640
VERSION     AV947640.1  GI:19425399
KEYWORDS    EST.
SOURCE      Ciona intestinalis.
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Ciona intestinalis"
                     /db_xref="taxon:7719"
                     /clone="ciad01g16"
                     /clone_lib="Nori Satoh unpublished cDNA library, young
                     adult"
                     /tissue_type="whole animal"
                     /dev_stage="young adult"
                     /note="Vector: pBluescript SK"
BASE COUNT        0 a      23 c       0 g      23 t       1 others
ORIGIN

  Query Match             1.5%;  Score 24.2;  DB 10;  Length 47;
  Best Local Similarity   69.6%;  Pred. No. 5.4e+05;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy      12 AGCGAGGGAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAG 57
           || ||| ||||||| ||| | | |||   ||| |||  || || ||
Db      46 AGAGAGAGAGAGAGAGAGAGAGAGANAGAGAGAGAGAGAGAGAG 1


RESULT 9
BJ000572/c
LOCUS       BJ000572                  45 bp    mRNA    linear   EST 05-DEC-2001
DEFINITION  BJ000572 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA019B12 5',
            mRNA sequence.
ACCESSION   BJ000572
VERSION     BJ000572.1  GI:17361239
KEYWORDS    EST.
SOURCE      Japanese medaka.
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
  TITLE     Medaka EST Project in Takeda's lab
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Oryzias latipes"
                     /strain="Hd-rR"
                     /db_xref="taxon:8090"
                     /clone="MF01SSA019B12"
                     /clone_lib="MF01SSA cDNA"
                     /sex="mixture of female and male"
                     /tissue_type="whole embryo"
                     /dev_stage="segmentation stage 20 - 25"
BASE COUNT        1 a      23 c       0 g      19 t       2 others
ORIGIN

  Query Match             1.5%;  Score 23.8;  DB 13;  Length 45;
  Best Local Similarity   68.9%;  Pred. No. 6.4e+05;
  Matches   31;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy      13 GCGAGGGAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAG 57
           | ||| ||||||| ||| | | |||   ||| |||  || || ||
Db      45 GNGAGNGAGAGAGAGAGAGTGAGAGAGAGAGAGAGAGAGAGAG 1


RESULT 10
AI701058
LOCUS       AI701058                  46 bp    mRNA    linear   EST 17-DEC-1999
DEFINITION  wc78c06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2324746 3'
            similar to WP:C18D11.4 CE18515 RNA RECOGNITION MOTIF. ;contains
            MER22.t3 MSR1 repetitive element ;, mRNA sequence.
ACCESSION   AI701058
VERSION     AI701058.1  GI:4988958
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 3363   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2324746"
                     /clone_lib="NCI_CGAP_Pan1"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.72 kb. Life Technologies catalog #:
                     11548-013"
BASE COUNT        8 a      8 c      30 g       0 t
ORIGIN

  Query Match             1.5%;  Score 23.8;  DB 9;  Length 46;
  Best Local Similarity   72.1%;  Pred. No. 6.4e+05;
```

```
  Matches   31;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy   1346 GGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCAGAG 1388
          ||||  ||||||| ||||| | |||| | ||||  | ||||
Db      2 GGGGGGGGCGGCGGAGGGGAGCCCGGGCGAGGCGCGAGAAGAG 44


RESULT 11
AV955412/c
LOCUS       AV955412                  47 bp    mRNA    linear   EST 14-MAR-2002
DEFINITION  AV955412 Nori Satoh unpublished cDNA library, egg Ciona
            intestinalis cDNA clone cieg08d15 5', mRNA sequence.
ACCESSION   AV955412
VERSION     AV955412.1  GI:19443711
KEYWORDS    EST.
SOURCE      Ciona intestinalis.
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Ciona intestinalis"
                     /db_xref="taxon:7719"
                     /clone="cieg08d15"
                     /clone_lib="Nori Satoh unpublished cDNA library, egg"
                     /tissue_type="whole animal"
                     /dev_stage="egg"
                     /note="Vector: pBluescript SK"
BASE COUNT        0 a     24 c      0 g     19 t      4 others
ORIGIN

  Query Match             1.5%;  Score 23.8;  DB 10;  Length 47;
  Best Local Similarity   66.0%;  Pred. No. 6.4e+05;
  Matches   31;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy      23 GAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGAG 69
           | | ||| | | |||   ||| |||  || || || |  ||||||||
Db      47 GNGNGAGAGNGNGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1


RESULT 12
AV949200/c
LOCUS       AV949200                  47 bp    mRNA    linear   EST 14-MAR-2002
DEFINITION  AV949200 Nori Satoh unpublished cDNA library, larva Ciona
            intestinalis cDNA clone cilv02g12 5', mRNA sequence.
ACCESSION   AV949200
VERSION     AV949200.1  GI:19437499
KEYWORDS    EST.
SOURCE      Ciona intestinalis.
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Ciona intestinalis"
                     /db_xref="taxon:7719"
                     /clone="cilv02g12"
                     /clone_lib="Nori Satoh unpublished cDNA library, larva"
                     /tissue_type="whole animal"
                     /dev_stage="larva"
                     /note="Vector: pBluescript SK"
BASE COUNT        1 a     23 c      0 g     23 t
ORIGIN

  Query Match             1.5%;  Score 23.6;  DB 10;  Length 47;
  Best Local Similarity   69.6%;  Pred. No. 7e+05;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy      12 AGCGAGGGAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAG 57
           || ||| ||||||| ||| | | |||   ||| |||  || || ||
Db      46 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1


RESULT 13
AZ385990/c
LOCUS       AZ385990                  47 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0144D16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0144D16 R, DNA sequence.
ACCESSION   AZ385990
VERSION     AZ385990.1  GI:10499690
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0144  row: D  column: 16
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 47.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0144D16"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
```

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 23 c 0 g 24 t
ORIGIN

Query Match 1.5%; Score 23.6; DB 17; Length 47;
Best Local Similarity 69.6%; Pred. No. 7e+05;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
Qy      12 AGCGAGGGAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAG 57
           || ||| ||||||| ||| | | |||   ||| |||  || || ||
Db      47 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2
```

RESULT 14
AZ853064/c
LOCUS AZ853064 47 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0156K04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0156K04 F, DNA sequence.
ACCESSION AZ853064
VERSION AZ853064.1 GI:13040804
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 47)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0156 row: K column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 47.
FEATURES Location/Qualifiers
source 1. .47
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0156K04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 23 c 0 g 24 t
ORIGIN

Query Match 1.5%; Score 23.6; DB 17; Length 47;
Best Local Similarity 69.6%; Pred. No. 7e+05;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 12 AGCGAGGGAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAG 57
|| ||| ||||||| ||| | | ||| ||| ||| || || ||
Db 47 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2

RESULT 15
AZ862836/c
LOCUS AZ862836 47 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0170N09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0170N09 R, DNA sequence.
ACCESSION AZ862836
VERSION AZ862836.1 GI:13060537
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 47)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0170 row: N column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 47.
FEATURES Location/Qualifiers
source 1. .47
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0170N09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
BASE COUNT        0 a      23 c       0 g      24 t
ORIGIN

  Query Match             1.5%;  Score 23.6;  DB 17;  Length 47;
  Best Local Similarity   69.6%;  Pred. No. 7e+05;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy      12 AGCGAGGGAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAG 57
           || ||| ||||||| ||| | | |||   ||| |||  || || ||
Db      47 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2


RESULT 16
AZ864870/c
LOCUS       AZ864870                 47 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0174M10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0174M10 R, DNA sequence.
ACCESSION   AZ864870
VERSION     AZ864870.1  GI:13064604
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0174  row: M  column: 10
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 47.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0174M10"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
```

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 23 c 0 g 24 t
ORIGIN

Query Match 1.5%; Score 23.6; DB 17; Length 47;
Best Local Similarity 69.6%; Pred. No. 7e+05;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 12 AGCGAGGGAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAG 57
|| ||| ||||||| ||| | | ||| ||| ||| || || ||
Db 47 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2

```
RESULT 17
AL676139
LOCUS       AL676139                 45 bp    mRNA    linear   EST 18-MAR-2002
DEFINITION  AL676139 XGC-gastrula Silurana tropicalis cDNA clone TGas053o17 5',
            mRNA sequence.
ACCESSION   AL676139
VERSION     AL676139.1  GI:19532513
KEYWORDS    EST.
SOURCE      western clawed frog.
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2002
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Taylor R
            Sanger Centre
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TGas053o17.p1cSP6
            Sequencing primer: P1CSP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Silurana tropicalis"
                     /db_xref="taxon:8364"
                     /clone="TGas053o17"
                     /clone_lib="XGC-gastrula"
                     /dev_stage="gastrula (stages 10.5-13 mixed)"
                     /lab_host="Escherichia coli XL1-blue"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from stages
                     10-13 gastrulae.  EcoRI-NotI cut cDNA was then ligated
                     into pCS107 with EcoRI at the 5' end and NotI at the 3'
                     end."
BASE COUNT        0 a      14 c      30 g       1 t
ORIGIN

  Query Match             1.5%;  Score 23.4;  DB 9;  Length 45;
  Best Local Similarity   73.2%;  Pred. No. 7.6e+05;
  Matches   30;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    1348 GGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCAGAG 1388
           || | ||||  |||||| |||  |||||||| | ||| | |
Db       3 GGGCGGCGGGTGCGGGGCCCGGCGGGGCGGCCGGGGCGGGG 43
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RESULT 18
AZ335579
LOCUS       AZ335579                 49 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0065A01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0065A01 R, DNA sequence.
ACCESSION   AZ335579
VERSION     AZ335579.1  GI:10404034
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0065  row: A  column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 49.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0065A01"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a      2 c     45 g      2 t
ORIGIN

  Query Match             1.5%;  Score 23.4;  DB 17;  Length 49;
  Best Local Similarity   81.8%;  Pred. No. 7.7e+05;
  Matches   27;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    1542 GCCGGGGGGCCGGGGGAGGGGCGCGGGAGGGGG 1574
           |||||||||  ||||| |||| | ||| |||||
Db      14 GCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 46
```

```
RESULT 19
BQ577141
LOCUS       BQ577141                 50 bp    mRNA    linear   EST 19-JUN-2002
DEFINITION  PfESToab14e02.y1 Plasmodium falciparum 3D7 asexual cDNA Plasmodium
            falciparum cDNA 5', mRNA sequence.
ACCESSION   BQ577141
VERSION     BQ577141.1  GI:21480458
KEYWORDS    EST.
SOURCE      malaria parasite P. falciparum.
  ORGANISM  Plasmodium falciparum
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D.,
            Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I.,
            Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A.,
            Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D.,
            Waterston,R., Wilson,R. and Sibley,D.
  TITLE     WashU Plasmodium EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: L. David Sibley
            WashU Plasmodium EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library was constructed by Debopam Chakrabarti DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: L. David Sibley
            (sibley@borcim.wustl.edu), Washington University
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Plasmodium falciparum"
                     /db_xref="taxon:5833"
                     /clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
                     /lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
                     /note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
                     XhoI; Library was constructed by Debopam Chakrabarti.
                     Total RNA samples were isolated from mixed stage
                     saponin(0.1%)-lysed P. falciparum 3D7 infected
                     erythrocytes by the acidic guanidinium-phenol chloroform
                     method. The poly A+ RNA was isolated by the polyAT-Tract
                     mRNA isolation system (Promega, WI) using streptavidin
                     Magnesphere particles. Directional cDNA libraries were
                     constructed by oligo d(T) priming of poly(A)+ RNA (5mg)
                     into EcoRI and XhoI sites of l ZapII vector using the Zap
                     cDNA synthesis kit (Stragene, CA). The average size of the
                     cDNA inserts in the library was between 1.0 and 1.5kb.
                     Clones were mass excised using the ExAssist helper phage
                     (Stratagene), the phagemids were precitptated with PEG
                     8000 and extracted with phenol/chloroform. Phagemid DNA
                     was electroporated into DH10B cells."
BASE COUNT       24 a      1 c     23 g      2 t
ORIGIN

  Query Match             1.5%;  Score 23.4;  DB 14;  Length 50;
  Best Local Similarity   67.3%;  Pred. No. 7.7e+05;
  Matches   33;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy      15 GAGGGAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAG 63
           ||| ||||||| ||| | | |||   ||| |||  || || ||  | ||
Db       1 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAACTAG 49


RESULT 20
AV672475/c
LOCUS       AV672475                 44 bp    mRNA    linear   EST 05-OCT-2000
DEFINITION  AV672475 Nori Satoh unpublished cDNA library Ciona intestinalis
            cDNA clone citb5m21 5', mRNA sequence.
ACCESSION   AV672475
VERSION     AV672475.1  GI:10110474
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```
KEYWORDS    EST.
SOURCE      Ciona intestinalis.
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Ciona intestinalis"
                     /db_xref="taxon:7719"
                     /clone="citb5m21"
                     /clone_lib="Nori Satoh unpublished cDNA library"
                     /tissue_type="whole animal"
                     /dev_stage="tailbud"
                     /note="Vector: pBluescript SK"
BASE COUNT        0 a     22 c      1 g     21 t
ORIGIN

  Query Match             1.5%;  Score 23.2;  DB 10;  Length 44;
  Best Local Similarity   70.5%;  Pred. No. 8.3e+05;
  Matches   31;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy      15 GAGGGAGAGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGC 58
           ||| ||||||| ||| | | |||   ||| |||  || || |||
Db      44 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1


RESULT 21
AA977986/c
LOCUS       AA977986                 49 bp    mRNA    linear   EST 26-MAY-1998
DEFINITION  oq55a06.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1590226 3'
            similar to TR:O00301 O00301 KSRP. ;contains element MER22
            repetitive element ;, mRNA sequence.
ACCESSION   AA977986
VERSION     AA977986.1  GI:3155432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1590226"
                     /clone_lib="NCI_CGAP_Kid5"
                     /tissue_type="2 pooled tumors (clear cell type)"
                     /lab_host="DH10B"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAATATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        0 a     24 c     18 g      7 t
ORIGIN

  Query Match             1.4%;  Score 22.6;  DB 9;  Length 49;
  Best Local Similarity   68.9%;  Pred. No. 1.1e+06;
  Matches   31;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    1339 CCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGCGGCGGCGG 1383
           ||| || |||||||| | || |||| | ||   |||| | || |
Db      47 CCGGGGGGGGGACAGGGCCGCCGGGAAACGGCCGGGCACCCGCCG 3


RESULT 22
AU103717/c
LOCUS       AU103717                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU103717 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HEP05140, mRNA sequence.
ACCESSION   AU103717
VERSION     AU103717.1  GI:13553238
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="HEP05140"
                     /clone_lib="Sugano Homo sapiens cDNA library"
                     /note="Differential display comparison of untreated and
                     dimethylfumarate treated U937 cells"
BASE COUNT        7 a     20 c     16 g      7 t
ORIGIN

  Query Match             1.4%;  Score 22.6;  DB 9;  Length 50;
  Best Local Similarity   86.2%;  Pred. No. 1.1e+06;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    1343 GGCGGGGACAGCGGCGGCGGGGACCGCGG 1371
           ||||| |||||||||||| |||  |||||
Db      37 GGCGGCGACAGCGGCGGCTGGGCTCGCGG 9
```

```
RESULT 23
BG078033
LOCUS       BG078033                 50 bp    mRNA    linear   EST 26-JAN-2001
DEFINITION  H3022G12-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
            H3022G12 5', mRNA sequence.
ACCESSION   BG078033
VERSION     BG078033.1  GI:12560601
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka
            ,T.S., Carter,M.G. and Ko,M.S.H.
  TITLE     Verification and initial annotation of NIA mouse 15K cDNA clone set
  JOURNAL   Unpublished (2001)
COMMENT     Other_ESTs: H3022G12-3
            Contact: George J. Kargul
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            This clone set has been freely distributed to the community. Please
            visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
            Plate: H3022  row: G  column: 12
            Seq primer: -21M13 Reverse
            High quality sequence stop: 50
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="niaEST:H3022G12-5"
                     /db_xref="taxon:10090"
                     /clone="H3022G12"
                     /clone_lib="NIA Mouse 15K cDNA Clone Set"
                     /sex="Clones arrayed from a variety of cDNA libraries"
                     /dev_stage="Clones arrayed from a variety of cDNA
                     libraries"
                     /lab_host="DH10B"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
                     clone is among a rearrayed set of 15,247 clones from 11
                     embryo  cDNA libraries (including preimplantation stage
                     embryos from  unfertilized egg to blastocyst, embryonic
                     part of E7.5 embryos,  extraembryonic part of E7.5 embryos
                     , and E12.5 female mesonephros/gonad)  and one newborn
                     ovary cDNA library. Average insert size 1.5 kb. All
                     source libraries are cloned unidirectionally with Oligo(dT
                     )-Not primers.  References include: (1) Genome-wide
                     expression profiling of mid-gestation  placenta and embryo
                     using a 15,000 mouse developmental cDNA microarray,  2000,
                     Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
                     Large-scale cDNA  analysis reveals phased gene expression
                     patterns during preimplantation  mouse develolpment, 2000,
                     Development, 127: 1737-1749; (3) Genome-wide  mapping of
                     unselected transcripts from extraembryonic tissue of
                     7.5-day  mouse embryos reveals enrichment in the t-complex
                     and under-representation  on the X chromosome, 1998, Hum
                     Mol Genet 7: 1967-1978."
BASE COUNT       18 a      0 c     31 g      1 t
ORIGIN

  Query Match             1.4%;  Score 22.4;  DB 12;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy     22 AGAGCGAGCGGGCGAGCCGGAGCGAGGAAGGGAAAGCGCAAGAGAGAG 69
          |||| | | ||  |||  |||| |||||||||   | |  || || ||
Db      3 AGAGAGGGAGGAAGAGAGGGAGGGAGGAAGGGGGTGGGAGAGGGAAAG 50


RESULT 24
```

```
BQ807914
LOCUS       BQ807914                 50 bp    mRNA    linear   EST 31-JUL-2002
DEFINITION  NISC_kk11g01.y1 NCI_CGAP_Brn72 Macaca mulatta cDNA clone
            IMAGE:5331264 5', mRNA sequence.
ACCESSION   BQ807914
VERSION     BQ807914.1  GI:22032123
KEYWORDS    EST.
SOURCE      rhesus monkey.
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM11840  row: N  column: 1
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Macaca mulatta"
                     /db_xref="taxon:9544"
                     /clone="IMAGE:5331264"
                     /clone_lib="NCI_CGAP_Brn72"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: brain; Vector: pCMV-SPORT6.ccdb; Site_1:
                     NotI; Site_2: EcoRV; Cloned unidirectionally. Primer:
                     Oligo dT. Average insert size 2.2 kb. Constructed by
                     Invitrogen. Note: this is a NCI_CGAP Library."
BASE COUNT       5 a     15 c     30 g      0 t
ORIGIN

  Query Match             1.4%;  Score 22.4;  DB 14;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   1328 GCGCGCACGGACCGCGGCGGGGACAGCGGCGGCGGGGACCGCGGGGGC 1375
          ||||||  |    |  || ||| ||||| ||| |||    ||||||||
Db      1 GCGCGCGGGCGGAGACGCCGGGGCAGCGCCGGAGGGCGGGGCGGGGGC 48


RESULT 25
BI547391
LOCUS       BI547391                 43 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603197282F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5276516 5',
            mRNA sequence.
ACCESSION   BI547391
VERSION     BI547391.1  GI:15434703
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
```

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            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM11698  row: d  column: 21
           High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5276516"
                     /clone_lib="NIH_MGC_95"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.5 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for  full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health).  Note: this is a NIH_MGC Library."
BASE COUNT        5 a      12 c      23 g       3 t
ORIGIN

  Query Match              1.4%;  Score 22.2;  DB 13;  Length 43;
  Best Local Similarity   77.1%;  Pred. No. 1.3e+06;
  Matches   27;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    1352 AGCGGCGGCGGGGACCGCGGGGGCGGCGGCGGCAG 1386
           ||||| |||||||  |||||| ||  |||||  ||
Db       1 AGCGGAGGCGGGGCGCGCGGGTGCACCGGCGTGAG 35


Search completed: March 13, 2003, 23:58:36
Job time : 2479 secs
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